514 Rec'd PCT/PTO 29 MAR 2000

FORM PTO-1390 (Modified) (REV 11-98) U.S. DEPARTMENT OF COMMERCE PATENT AND TRADEMARK OFFICE

TRANSMITTAL LETTER TO THE UNITED STATES DESIGNATED/ELECTED OFFICE (DO/EO/US) CONCERNING A FILING UNDER 35 U.S.C. 371

ATTORNEY'S DOCKET NUMBER: **5650-01-MJA**

U.S. APPLICATION NO. (IF KNOWN, SEE 37 CFR 1.5): **60/068179** 09/509779

INTERNATIONAL APPLICATION NO.	INTERNATIONAL FILING DATE	PRIORITY DATE CLAIMED
PCT/US98/26705	**December 15, 1998**	**December 19, 1997**

TITLE OF INVENTION

SAG: SENSITIVE TO APOPTOSIS GENE

APPLICANT(S) FOR DO/EO/US

SUN, Yi

Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information:

1. ☒ This is a **FIRST** submission of items concerning a filing under 35 U.S.C. 371.
2. ☐ This is a **SECOND** or **SUBSEQUENT** submission of items concerning a filing under 35 U.S.C 371.
3. ☒ This is an express request to begin national examination procedures (35 U.S.C. 371(f)) at any time rather than delay examination until the expiration of the applicable time limit set in 35 U.S.C. 371(b) and PCT Articles 22 and 39(1).
4. ☒ A proper Demand for International Preliminary Examination was made by the 19th month from the earliest claimed priority date.
5. ☒ A copy of the International Application as filed (35 U.S.C. 371 (c) (2))
   a. ☐ is transmitted herewith (required only if not transmitted by the International Bureau).
   b. ☐ has been transmitted by the International Bureau.
   c. ☒ is not required, as the application was filed in the United States Receiving Office (RO/US).
6. ☐ A translation of the International Application into English (35 U.S.C. 371(c)(2)).
7. ☒ A copy of the International Search Report (PCT/ISA/210).
8. ☒ Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. 371 (c)(3))
   a. ☐ are transmitted herewith (required only if not transmitted by the International Bureau).
   b. ☐ have been transmitted by the International Bureau.
   c. ☐ have not been made; however, the time limit for making such amendments has NOT expired.
   d. ☒ have not been made and will not be made.
9. ☐ A translation of the amendments to the claims under PCT Article 19 (35 U.S.C. 371(c)(3)).
10. ☒ An oath or declaration of the inventor(s) (35 U.S.C. 371 (c)(4)).
11. ☒ A copy of the International Preliminary Examination Report (PCT/IPEA/409)
12. ☐ A translation of the annexes to the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. 371 (c)(5)).

Items 13 to 20 below concern document(s) or information included:

13. ☒ An Information Disclosure Statement under 37 CFR 1.97 and 1.98.
14. ☐ An assignment document for recording. A separate cover sheet in compliance with 37 CFR 3.28 and 3.31 is included.
15. ☐ A **FIRST** preliminary amendment.
16. ☐ A **SECOND** or **SUBSEQUENT** preliminary amendment.
17. ☐ A substitute specification.
18. ☐ A change of power of attorney and/or address letter.
19. ☒ Certificate of Mailing by Express Mail
20. ☐ Other items or information:

Express Mail No. EJ676053129US
PD-5650-01-MJA

PCTUS1/REV03

09/509779

U.S. APPLICATION NO. (IF KNOWN, SEE 37 CFR 1.5)	INTERNATIONAL APPLICATION NO.	ATTORNEY'S DOCKET NUMBER
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21. The following fees are submitted:.

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BASIC NATIONAL FEE (37 CFR 1.492 (a) (1) - (5)) :	CALCULATIONS	PTO USE ONLY
☒ Neither international preliminary examination fee (37 CFR 1.482) nor international search fee (37 CFR 1.445(a)(2) paid to USPTO and International Search Report not prepared by the EPO or JPO $970.00		
☐ International preliminary examination fee (37 CFR 1.482) not paid to USPTO but Internation Search Report prepared by the EPO or JPO $840.00		
☐ International preliminary examination fee (37 CFR 1.482) not paid to USPTO but international search fee (37 CFR 1.445(a)(2)) paid to USPTO $690.00		
☐ International preliminary examination fee paid to USPTO (37 CFR 1.482) but all claims did not satisfy provisions of PCT Article 33(1)-(4) $670.00		
☐ International preliminary examination fee paid to USPTO (37 CFR 1.482) and all claims satisfied provisions of PCT Article 33(1)-(4) $96.00		
ENTER APPROPRIATE BASIC FEE AMOUNT =	**$970.00**	
Surcharge of **$130.00** for furnishing the oath or declaration later than ☐ 20 ☐ 30 months from the earliest claimed priority date (37 CFR 1.492 (e)).	**$0.00**	

CLAIMS	NUMBER FILED	NUMBER EXTRA	RATE		
Total claims	37 - 20 =	17	x $18.00	**$306.00**	
Independent claims	17 - 3 =	14	x $78.00	**$1,092.00**	
Multiple Dependent Claims **(check if applicable)**.			☒	**$260.00**	
	TOTAL OF ABOVE CALCULATIONS =			**$2,628.00**	
Reduction of 1/2 for filing by small entity, if applicable. Verified Small Entity Statement must also be filed (Note 37 CFR 1.9, 1.27, 1.28) **(check if applicable).** ☐				**$0.00**	
	SUBTOTAL =			**$2,628.00**	
Processing fee of **$130.00** for furnishing the English translation later than ☐ 20 ☐ 30 months from the earliest claimed priority date (37 CFR 1.492 (f)). +				**$0.00**	
	TOTAL NATIONAL FEE =			**$2,628.00**	
Fee for recording the enclosed assignment (37 CFR 1.21(h)). The assignment must be accompanied by an appropriate cover sheet (37 CFR 3.28, 3.31) **(check if applicable).** ☐				**$0.00**	
	TOTAL FEES ENCLOSED =			**$2,628.00**	
				Amount to be: refunded	$
				charged	$

☐ A check in the amount of to cover the above fees is enclosed.

☒ Please charge my Deposit Account No. **23-0455** in the amount of **$2,628.00** to cover the above fees.
A duplicate copy of this sheet is enclosed.

☒ The Commissioner is hereby authorized to charge any fees which may be required, or credit any overpayment to Deposit Account No. **23-0455** A duplicate copy of this sheet is enclosed.

NOTE: Where an appropriate time limit under 37 CFR 1.494 or 1.495 has not been met, a petition to revive (37 CFR 1.137(a) or (b)) must be filed and granted to restore the application to pending status.

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3/29/00
DATE

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CERTIFICATE OF MAILING BY "EXPRESS MAIL" (37 CFR 1.10) Applicant(s): Yi Sun			Docket No. 5750-01-TMC
Serial No. 09/509779	Filing Date	Examiner	Group Art Unit

Invention: **METHOD OF INHIBITING METASTASES OF CANCER CELLS**

I hereby certify that this **Application for filing under 35 U.S.C. 371**
(Identify type of correspondence)
is being deposited with the United States Postal Service "Express Mail Post Office to Addressee" service under 37 CFR 1.10 in an envelope addressed to: The Assistant Commissioner for Patents, Washington, D.C. 20231

on **March 29, 2000**
(Date)

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PD-5650-01-MJA

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SAG: SENSITIVE TO APOPTOSIS GENE

Background of the Invention

The present invention relates to a novel gene and polypeptides derived therefrom encoding a redox-sensitive protein that protects cells from apoptosis and promotes cell growth, as well as antibodies directed against the polypeptide. The invention also describes methods for using the novel gene, polypeptides, and antibodies in the detection of genetic deletions of the gene, subcellular localization of the polypeptide, isolation of discrete classes of RNA, inhibition of apoptosis, scavenging of oxygen radicals, reversion of tumor phenotype, and therapeutic applications by gene therapy.

Summary of the Related Art

Apoptosis, also referred to as programmed cell death, is a genetically programmed process for maintaining homeostasis under physiological conditions and for responding to various stimuli (Thompson (1995) Science 267, 1456-1462). This form of cell death is characterized by cell membrane blebbing, cytoplasmic shrinkage, nuclear chromatin condensation, and DNA fragmentation (Wyllie (1980) Int. Rev. Cytol. 68, 251-306). The process of apoptosis can be divided into three distinct phases: initiation, effector molecule stimulation and DNA degradation (Kroemer et al. (1995) FASEB J. 9, 1277-1287; Vaux and Strasser (1996) Proc. Natl. Acad. Sci. USA 93, 2239-2244). Apoptosis can be initiated in various cell types by a wide variety of physical, chemical, and biological stimuli (both internal and external), including diverse cancer therapeutic drugs, oxidative DNA damage reagents, and cytokines (Kroemer (1997) Nature Med. 3, 614-620, White (1996) Genes Dev. 10, 1-15; Sen and D'Incalci (1992) FEBS Lett. 307, 122-127; Dive and Hickman (1991) Br. J. Cancer 64, 192-196; Yuan et al. (1993) Cell 75, 641-652). These initiators trigger the effector molecules in cells leading to apoptotic signal transduction and amplification, which ultimately results in irreversible DNA degradation and cell death.

Many genes are involved in the apoptotic process. In general, the products of these genes are classified as either inducers or inhibitors of apoptosis. The balance between the activities of apoptosis inducers and inhibitors in a given cell determines whether that cell undergoes apoptosis. Among the growing list of apoptotic regulatory genes, the most well characterized are the p53 tumor suppressor gene, the Bcl-2 gene family (consisting of both inducers and inhibitors of apoptosis), the interleukin 1β converting enzyme (ICE) gene family, and FAS/Fas ligand (Kroemer (1997), White (1996); Yuan et al. (1993); Nagata and

Golstein (1995) Science 267, 1449-1456). During apoptosis, there are substantial interactions involving the products of apoptotic regulatory genes, including heterodimer formation among the gene products of the Bcl-2 gene family, and p53 activation of Bax expression (Oltvai et al. (1993) Cell 74, 609-619; Miyashita and Reed (1995) Cell 80, 293-299).

The inventor has recently found that 1,10 phenanthroline ("OP"), a metal chelating agent, can activate p53 activity and induce apoptosis in two murine tumor cell lines that harbor endogenous wild-type p53 (Sun et al. (1997) Oncogene 14, 385-393). OP is a typical metal chelating reagent in that it chelates Fe(II) and prevents Fe(II)-mediated hydroxyl radical formation through the Fenton reaction (Halliwell et al. (1989) in: Free Radicals in Biology and Medicine, 2nd ed., Clarendon Press, Oxford; Auld (1988) in Methods in Enzymology, Vol. 158 (J. F. Riordan and B. L. Valle, Eds.) PP. 110-114, Academic Press, New York). OP has been shown to prevent hydroxyl radical-induced DNA damage in a number of cellular systems (Sun, Y. Free Radic. Biol. Med. 8:583-599 (1990); Martins and Meneghini, Biochem J. 299:137-140 (1994); Morgan et al., Biochem. Pharmacol. 44:215-221 (1992)). Activation of p53 by OP was found to significantly contribute to, but was not required for subsequent apoptotic cell death (Sun et al., (1997) Oncogene 14: 385-393; Sun (1997) FEBS Lett. 408, 16-20). Thus, the critical genes and gene products responsible for OP-induced apoptosis remain to be characterized. A better understanding of the molecular mechanisms of apoptotic induction will allow improved design of therapeutic drugs that either induce (anti-cancer) or inhibit (anti-aging) apoptosis.

Summary of the Invention

The present invention provides novel genes and polypeptides derived therefrom encoding a redox-sensitive protein that protects cells from apoptosis, scavenges oxygen radicals, and can be used for the reversion of a tumor phenotype.

In one aspect, the present invention provides novel isolated and purified DNA sequences (referred to herein as "mouse SAG" and "human SAG") as shown in SEQ ID 1 and SEQ ID 3, and their gene products (referred to herein as "mouse SAG protein" and "human SAG protein") as shown in SEQ ID 2 and SEQ ID 4, that are induced during 1,10-phenanthroline ("OP")-induced apoptosis. In another embodiment, the present invention comprises a nucleotide sequence that hybridizes to the nucleotide sequence shown in SEQ ID 1 and SEQ ID 3 under high stringency hybridization conditions. In a preferred embodiment, the isolated and purified DNA sequence consists essentially of the DNA sequence of SEQ ID 1 or SEQ ID 3.

In another aspect, the invention provides novel recombinant DNA molecules, comprising SAG subcloned into an extra-chromosomal vector. In a further aspect, the present invention provides recombinant host cells that are stably transfected with a recombinant DNA molecule comprising SAG subcloned into an extra-chromosomal vector.

In a different aspect, the present invention provides a substantially purified recombinant protein comprising a polypeptide substantially similar to the SAG protein shown in SEQ ID 2 and SEQ ID 4. In a further aspect, the present invention provides a polyclonal antibody that selectively binds to proteins with an amino acid sequence substantially similar to the amino acid sequence shown in SEQ ID 2 and SEQ ID 4.

Additional aspects of the present invention provide a method of detecting the SAG protein in cells, comprising contacting cells with a polyclonal antibody that recognizes the SAG protein; a method of detecting cells containing SAG deletions, comprising isolating total genomic DNA from the cell and subjecting the genomic DNA to PCR amplification using primers derived from the DNA sequence of SEQ ID 1 and SEQ ID 3; and a method of detecting cells containing SAG deletions, comprising isolating total cell RNA and subjecting the RNA to reverse transcription-PCR amplification using primers derived from the DNA sequence of SEQ ID 1 and SEQ ID 3.

In another aspect, the present invention further provides methods of isolating RNA containing stretches of polyA, polyC, or polyU residues from cells, contacting the total cell RNA with the SAG protein, and incubating the RNA-SAG protein mixture with an antibody that recognizes the SAG protein.

In another aspect of the present invention, a method for isolating genes induced during cell apoptosis is provided, comprising treating cells with OP, subjecting the OP-induced RNA to the differential display procedure, and cloning the OP-induced genes.

A further aspect of the invention provides a method for protecting mammalian and/or non-mammalian cells from apoptosis induced by redox reagents, comprising introducing into mammalian and/or non-mammalian cells an expression vector comprising a DNA sequence substantially similar to the DNA sequence shown in SEQ ID 1 and SEQ ID 3, which is operatively linked to a DNA sequence that promotes the expression of the DNA sequence, wherein the isolated and purified DNA sequence of SEQ ID 1 and SEQ ID 3 will be expressed at high levels in the mammalian and/or non-mammalian cells.

An additional aspect of the present invention provides a method for treatment of mammalian and/or non-mammalian tumor cells, comprising introducing into mammalian and/or non-mammalian tumor cells an expression vector comprising a DNA sequence

substantially similar to the DNA sequence shown in SEQ ID 1 and SEQ ID 3, which is operatively linked to a DNA sequence that promotes the expression of the antisense strand of the DNA sequence, wherein the antisense strand of the DNA sequence of SEQ ID 1 and SEQ ID 3 will be expressed at high levels in the mammalian and/or non-mammalian cells.

Another aspect of the present invention provides a method for oxygen radical scavenging in an organism, comprising administering an oxygen radical-reducing amount of a pharmaceutical composition comprising SAG protein and a pharmaceutically acceptable carrier.

A further aspect of the present invention provides for gene therapy applications of SAG, including but not limited to methods of promoting the closure (i.e., healing) of a wound in a patient.

The foregoing is not intended and should not be construed as limiting the invention in any way. All patents and publications cited herein are incorporated by reference in their entirety.

Brief Description of the Drawings

Figure 1A. Predicted structural features of the deduced protein sequence of the mouse and human SAG cDNA.

Figure 1B. Description of human SAG protein mutants.

Figure 2. Bar graph depiction of soft agar colony growth of various SAG-transfected stable cell lines.

Figure 3. Graphical representation of tumor mass in SCID mice per days post implant with SAG transfectants.

Detailed Description of the Invention

The present invention provides novel genes and polypeptides derived therefrom encoding a redox-sensitive protein that protects cells from apoptosis, scavenges oxygen radicals, and can be used for the reversion of a tumor phenotype. The present invention also comprises genes and their gene products involved in OP-induced apoptosis. The isolation of such genes and their gene products permits a detailed analysis of the OP-induced apoptotic pathway, thus providing laboratory tools useful to identify the mechanisms of OP-induced apoptosis and enabling improved design of therapeutic drugs to regulate apoptosis.

Within this application, unless otherwise stated, the techniques utilized may be found in any of several well-known references such as: *Molecular Cloning: A Laboratory Manual*

(Sambrook, et al., 1989, Cold Spring Harbor Laboratory Press), *Gene Expression Technology* (Methods in Enzymology, Vol. 185, edited by D. Goeddel, 1991. Academic Press, San Diego, CA), "Guide to Protein Purification" in *Methods in Enzymology* (M.P. Deutshcer, ed., (1990) Academic Press, Inc.); *PCR Protocols: A Guide to Methods and Applications* (Innis, et al. 1990. Academic Press, San Diego, CA), *Culture of Animal Cells: A Manual of Basic Technique, 2nd Ed.* (R.I. Freshney. 1987. Liss, Inc. New York, NY), and *Gene Transfer and Expression Protocols*, pp. 109-128, ed. E.J. Murray, The Humana Press Inc., Clifton, N.J.).

In one aspect, the present invention provides novel isolated and purified DNA sequences, hereinafter referred to as Sensitive to Apoptosis Genes ("SAG"), encoding SAG proteins. In one embodiment, the invention comprises DNA sequences substantially similar to those shown in SEQ ID 1 (mouse SAG) or SEQ ID 2 (human SAG), respectively. As defined herein, "substantially similar" includes identical sequences, as well as deletions, substitutions or additions to a DNA, RNA or protein sequence that maintain the function of the protein product and possess similar zinc-binding motifs. Preferably, the DNA sequences according to the invention consist essentially of the DNA sequence of SEQ ID 1 or SEQ ID 3, or are selected from the group consisting of SEQ ID 11, SEQ ID 13, SEQ ID 21, SEQ ID 23, SEQ ID 25, SEQ ID 27, SEQ ID 29, SEQ ID 31, SEQ ID 33, SEQ ID 35, SEQ ID 37, SEQ ID 39, SEQ ID 41, SEQ ID 43, SEQ ID 45, SEQ ID 47 and SEQ ID 49. These novel purified and isolated DNA sequences can be used to direct expression of the SAG protein and for mutational analysis of SAG protein function.

Mutated sequences according to the invention can be identified in a routine manner by those skilled in the art using the teachings provided herein, as described in Example 8, *infra*, and techniques well known in the art.

In another embodiment, the invention comprises a nucleotide sequence that hybridizes to SEQ ID 1 and/or SEQ ID 3 under high stringency hybridization conditions. As used herein, the term "high stringency hybridization conditions" refers to hybridization at 65°C in a low salt hybridization buffer to the probe of interest at 2 x 10^8 cpm/μg for between about 8 hours to 24 hours, followed by washing in 1% SDS, 20 mM phosphate buffer and 1 mM EDTA at 65°C, for between about 30 minutes to 4 hours. In a preferred embodiment, the low salt hybridization buffer comprises between, 0.5-10% SDS, and 0.05M and 0.5 M sodium phosphate. In a most preferred embodiment, the low salt hybridization buffer comprises, 7% SDS, and 0.125M sodium phosphate. These DNA sequences can be used to direct expression

of the SAG protein and for mutational analysis of SAG protein function, and are isolated via hybridization as described.

In another aspect, the invention provides novel recombinant DNA molecules, comprising SAG or a sequence substantially similar to it subcloned into an extra-chromosomal vector. This aspect of the invention allows for *in vitro* expression of the SAG gene, thus permitting an analysis of SAG gene regulation and SAG protein structure and function. As used herein, the term "extra-chromosomal vector" includes, but is not limited to, plasmids, bacteriophages, cosmids, retroviruses and artificial chromosomes. In a preferred embodiment, the extra-chromosomal vector comprises an expression vector that allows for SAG protein production when the recombinant DNA molecule is inserted into a host cell. Such vectors are well known in the art and include, but are not limited to, those with the T3 or T7 polymerase promoters, the SV40 promoter, the CMV promoter, or any promoter that either can direct gene expression, or that one wishes to test for the ability to direct gene expression. These recombinant vectors are produced via standard recombinant DNA protocols as described in the references cited above. This aspect of the invention allows for high level expression of the SAG protein.

In a further aspect, the present invention provides recombinant host cells that are stably transfected with a recombinant DNA molecule comprising SAG subcloned into an extra-chromosomal vector. The host cells of the present invention may be of any type, including, but not limited to, non-eukaryotic (e.g., bacterial), and eukaryotic such as fungal (e.g., yeast), plant, non-human animal, non-human mammalian (e.g., rabbit, porcine, mouse, horse) and human cells. Transfection of host cells with recombinant DNA molecules is well known in the art (Sambrook et al., Molecular Cloning, A Laboratory Manual, 2nd ed., Cold Spring Harbor Press, 1989) and, as used herein, includes, but is not limited to calcium phosphate transfection, dextran sulfate transfection, electroporation, lipofection and viral infection. This aspect of the invention allows for *in vitro* and *in vivo* expression of SAG and its gene product, thus enabling high-level expression of SAG protein, as described in Example 6, *infra*.

In another aspect, the present invention provides a substantially purified recombinant protein comprising a polypeptide substantially similar to the SAG polypeptides shown in SEQ ID 2 and SEQ ID 4. Furthermore, this aspect of the invention enables the use of SAG protein in several *in vitro* assays described below. As used herein, the term "substantially similar" includes deletions, substitutions and additions to the sequences of SEQ IDs 1-4 (as

appropriate) introduced by any *in vitro* means. As used herein, the term "substantially purified" means that the protein should be free from detectable contaminating protein, but the SAG protein may be co-purified with an interacting protein, or as an oligomer. Preferably, the protein sequences according to the invention comprise an amino acid sequence selected from the group consisting of SEQ ID 2, SEQ ID 4, SEQ ID 12, SEQ ID 14, SEQ ID 22, SEQ ID 24, SEQ ID 26, SEQ ID 28, SEQ ID 30, SEQ ID 32, SEQ ID 34, SEQ ID 36, SEQ ID 38, SEQ ID 40, SEQ ID 42, SEQ ID 44, SEQ ID 46, SEQ ID 48, and SEQ ID 50. In a most preferred embodiment, the protein sequences according to the invention comprise an amino acid sequence selected from the group consisting of SEQ ID 2 and SEQ ID 4. Mutated sequences according to the invention can be identified in a routine manner by those skilled in the art using the teachings provided herein and techniques well known in the art. This aspect of the invention provides a novel purified protein that can be used for *in vitro* assays, as described in Examples 12, *infra*, and as a component of a pharmaceutical composition for oxygen radical scavenging, described *infra*.

In a further aspect, the present invention provides antibodies and methods for detecting antibodies that selectively bind polypeptides with an amino acid sequence substantially similar to the amino acid sequence of SEQ ID 2 and SEQ ID 4. The antibody of the present invention can be a polyclonal or a monoclonal antibody, prepared by using all or part of the sequence of SEQ ID 2 or SEQ ID 4, or modified portions thereof, to elicit an immune response in a host animal according to standard techniques (Harlow and Lane (1988), eds. Antibody: A Laboratory Manual, Cold Spring Harbor Press). In a preferred embodiment, the entire polypeptide sequence of SEQ ID 2 or SEQ ID 4 is used to elicit the production of polyclonal antibodies in a host animal.

The method of detecting SAG antibodies comprises contacting cells with an antibody that recognizes SAG protein and incubating the cells in a manner that allows for detection of the SAG protein-antibody complex. Standard conditions for antibody detection of antigen can be used to accomplish this aspect of the invention (Harlow and Lane, 1988). This aspect of the invention permits the detection of SAG protein both *in vitro* and *in vivo*, as described in Examples 12 and 14, *infra*.

In a further aspect, the present invention provides a diagnostic assay for detecting cells containing SAG deletions, comprising isolating total genomic DNA from the cell and subjecting the genomic DNA to PCR amplification using primers derived from the DNA sequence of SEQ ID 1 SEQ ID 3, SEQ ID 11, SEQ ID 13, SEQ ID 21, SEQ ID 23, SEQ

ID 25, SEQ ID 27, SEQ ID 29, SEQ ID 31, SEQ ID 33, SEQ ID 35, SEQ ID 37, SEQ ID 39, SEQ ID 41, SEQ ID 43, SEQ ID 45, SEQ ID 47 and SEQ ID 49.

This aspect of the invention enables the detection of SAG deletions in any type of cell, and can be used in genetic testing or as a laboratory tool. The PCR primers can be chosen in any manner that allows the amplification of a SAG gene fragment large enough to be detected by gel electrophoresis. Detection can be by any method, including, but not limited to ethidium bromide staining of agarose or polyacrylamide gels, autoradiographic detection of radio-labeled SAG gene fragments, Southern blot hybridization, and DNA sequence analysis. In a preferred embodiment, detection is accomplished by polyacrylamide gel electrophoresis, followed by DNA sequence analysis to verify the identity of the deletions. PCR conditions are routinely determined based on the length and base-content of the primers selected according to techniques well known in the art (Sambrook et al., 1989).

An additional aspect of the present invention provides a diagnostic assay for detecting cells containing SAG deletions, comprising isolating total cell RNA and subjecting the RNA to reverse transcription-PCR amplification using primers derived from the DNA sequence of SEQ ID 1 SEQ ID 3, SEQ ID 11, SEQ ID 13, SEQ ID 21, SEQ ID 23, SEQ ID 25, SEQ ID 27, SEQ ID 29, SEQ ID 31, SEQ ID 33, SEQ ID 35, SEQ ID 37, SEQ ID 39, SEQ ID 41, SEQ ID 43, SEQ ID 45, SEQ ID 47 and SEQ ID 49. This aspect of the invention enables the detection of SAG deletions in any type of cell, and can be used in genetic testing or as a laboratory tool.

Reverse transcription is routinely accomplished via standards techniques (Ausubel et al., in Current Protocols in Molecular Biology, ed. John Wiley and Sons, Inc., 1994) and PCR is accomplished as described above.

In another aspect, the present invention provides methods of isolating RNA containing stretches of polyA (adenine), polyC (cytosine) or polyU (uridine) residues, comprising contacting an RNA sample with SAG protein, incubating the RNA-SAG protein mixture with an antibody that recognizes the SAG polypeptide, isolating the antibody-SAG protein-RNA complexes, and purifying the RNA away from the antibody-SAG protein complex. This aspect of the invention provides a novel *in vitro* method for isolating a discrete class of RNA. In a preferred embodiment, the RNA sample is contacted with SAG protein in the presence (for preferential isolation of polyA and polyC-containing RNAs), or absence (for preferential isolation of polyU-containing RNAs), of a reducing agent. Preferred reducing agents for use in this aspect of the invention include, but are not limited to DTT and

β-mercaptoethanol. The reducing agents are preferably used at a concentration of between about 50 mM and 1 M. Isolation of antibody-SAG protein-RNA complexes can be accomplished via standard techniques in the art, including, but not limited to the use of Protein-A conjugated to agarose or cellulose beads.

In a further aspect of the present invention, a method for isolating genes induced during cell apoptosis is provided, comprising treating one set of cells with OP and not treating a control set of cells, isolating RNA from each set of cells, subjecting the RNA from each set of cells to reverse transcription and PCR ("differential display"), identifying cDNAs that are expressed in the OP-treated set of cells and not in the control set of cells, and cloning the OP-induced cDNAs. This aspect of the invention provides a tool for isolating other genes that control the OP-induced apoptotic pathway and is useful both as a way to enable the design of therapeutic drugs that regulate apoptosis and as a laboratory tool to identify the mechanisms of OP-induced apoptosis. Details of the differential display technique, including selection of primers, are well known in the art (Liang and Pardee, Science 257:967-971, 1992). Reverse transcription and PCR conditions are routinely determined based on the length and base-content of the primers selected according to techniques well known in the art (Sambrook et al., 1989). In a preferred embodiment, OP is used at a concentration of between 50 μM and 300 μM. In a most preferred embodiment, OP is used at a concentration of between 100 μM and 150 μM.

A further aspect of the invention provides a method for protecting mammalian and/or non-mammalian cells from apoptosis induced by redox reagents, comprising introducing into mammalian and/or non-mammalian cells an expression vector comprising a DNA sequence substantially similar to the DNA sequence shown in SEQ ID 1 or SEQ ID 3, that is operatively linked to a DNA sequence that promotes the expression of the DNA sequence and incubating the cells under conditions wherein the DNA sequence of SEQ ID 1 or SEQ ID 3 will be expressed at high levels in the mammalian and/or non-mammalian cells. In a preferred embodiment, the DNA sequence consist essentially of SEQ ID 1 or SEQ ID 3. Suitable expression vectors are as described above. In a preferred embodiment, the coding region of the human SAG gene is subcloned into an expression vector under the transcriptional control of the cytomegalovirus (CMV) promoter to allow for constitutive SAG gene expression.

An additional aspect of the present invention provides a method for inhibiting the growth of mammalian and/or non-mammalian tumor cells, comprising introducing into

mammalian and/or non-mammalian tumor cells an expression vector comprising a DNA that is antisense to a sequence substantially similar to the DNA sequence shown in SEQ ID 1 or SEQ ID 3 that is operatively linked to a DNA sequence that promotes the expression of the antisense DNA sequence. The cells are then grown under conditions wherein the antisense DNA sequence of SEQ ID 1 or SEQ ID 3 will be expressed at high levels in the mammalian and/or non-mammalian cells. In a preferred embodiment, the DNA sequence consists essentially of SEQ ID 1, SEQ ID 3, SEQ ID 11, SEQ ID 13, SEQ ID 21, SEQ ID 23, SEQ ID 25, SEQ ID 27, SEQ ID 29, SEQ ID 31, SEQ ID 33, SEQ ID 35, SEQ ID 37, SEQ ID 39, SEQ ID 41, SEQ ID 43, SEQ ID 45, SEQ ID 47 and SEQ ID 49.

In a most preferred embodiment, the DNA sequence consists essentially of SEQ ID 1 or SEQ ID 3. In a further preferred embodiment, the expression vector comprises an adenoviral vector wherein SAG cDNA is operatively linked in an antisense orientation to a cytomegalovirus (CMV) promoter to allow for constitutive expression of the SAG antisense cDNA in a host cell. In a preferred embodiment, the SAG adenoviral expression vector is introduced into mammalian tumor cells by injection into a mammalian tumor cell mass.

An additional aspect of the present invention provides a method for oxygen radical scavenging in an organism, comprising introducing into mammalian and/or non-mammalian cells an expression vector comprising a DNA sequence substantially similar to the DNA sequence shown in SEQ ID 1 or SEQ ID 3 which is operatively linked to a DNA sequence that promotes the expression of the DNA sequence, and the cells are grown under conditions wherein the DNA sequence of SEQ ID 1 or SEQ ID 3 will be expressed at high levels in the mammalian and/or non-mammalian cells. In a preferred embodiment, the DNA sequence consists essentially of SEQ ID 1 or SEQ ID 3. In a preferred embodiment, the SAG cDNA is operatively linked to a cytomegalovirus (CMV) promoter, to allow for constitutive expression of the SAG cDNA in a host cell.

Another aspect of the present invention provides pharmaceutical compositions and methods for oxygen radical scavenging in an organism, comprising administering an oxygen-reducing amount of a pharmaceutical composition comprising the SAG protein of SEQ ID 2 or SEQ ID 4 and a pharmaceutically acceptable carrier.

Chimeric gene constructs of the present invention (e.g., expression vectors) containing SAG polynucleotide sequences may be used in gene therapy applications to achieve expression of SAG or anti-sense SAG polynucleotide sequences in selected target cells, including non-eukaryotic cells (i.e., plant) and eukaryotic cells. Gene therapy applications typically involve identifying target host cells or tissues in need of the therapy,

designing vector constructs capable of expressing a desired gene product in the identified cells, and delivering the constructs to the cells in a manner that results in efficient transduction of the target cells.

The cells or tissues targeted by gene therapy are typically those that are affected by the disease that the vector construct is designed to treat. For example, in the case of cancer, the targeted tissues are malignant tumors.

In one embodiment, the present invention provides a method of promoting the closure (i.e., healing) of a wound in a patient. This method involves transferring exogenous SAG to the region of the wound whereby a product of SAG is produced in the region of the wound to promote the closure (i.e., healing) of the wound.

The present inventive method promotes closure (i.e., healing) of both external (e.g., surface) and internal wounds. Wounds to which the present inventive method is useful in promoting closure (e.g., healing) include, but are not limited to, abrasions, avulsions, blowing wounds, burn wounds, contusions, gunshot wounds, incised wounds, open wounds, penetrating wounds, perforating wounds, puncture wounds, seton wounds, stab wounds, surgical wounds, subcutaneous wounds, tangential wounds, or traumatopneic wounds. Preferably, the present inventive methods are employed to close chronic open wounds, such as non-healing external ulcers and the like.

Exogenous SAG can be introduced into the region of the wound by any appropriate means, such as, for example, those means described herein. For example, where the wound is a surface wound, SAG can be supplied exogenously by topical administration of SAG protein to the region of the wound.

Preferably, exogenous SAG is provided to the wound by transferring a vector comprising an SAG expression cassette to cells associated with the wound. Upon expression of SAG within the cells in the region of the wound, a product of SAG is produced to promote wound closure (i.e., healing). Transferring a vector comprising an SAG expression cassette to cells associated with the wound is preferred as such procedure is minimally invasive, supplies SAG products locally within the region of the wound, and requires no reapplication of salves, solutions, or other extrinsic media. Furthermore, SAG activity remains expressed during wound closure and will inactivate following healing.

The vector comprising the SAG expression cassette can be transferred to the cells associated with the wound in any manner appropriate to transfer the specific vector type to the cells, such as those methods discussed herein.

As discussed above, the cells associated with the wound to which the vector is transferred are any cells sufficiently connected with the wound such that expression of SAG within those cells promotes wound closure (i.e., healing), such as cells within the wound or cells from other sources. In one embodiment, the cells are cells of the wound, and the present inventive method comprises transfer of the vector to the cells *in situ*.

In other embodiments, the cells are not the cells of the wound, but can be cells in an exogenous tissue, such as a graft, or can be cells *in vitro*. For example, to promote the healing of certain types of wounds, the cells associated with the wound can be cells within a graft, such as a skin graft. Transfer of the vector to the cells associated with the wound, thus involves transferring the vector to the cells within the graft *ex vivo*. For other wounds, the cells associated with the wound are cells *in vitro*, and the cells are transferred to the region of the wound following transfer to them of a vector containing the SAG expression cassette.

The present inventive method applies to any patient having a wound. For example, the patient can be any animal, such as a mammal. Preferably, the patient is human.

In another embodiment, the present invention provides a method of inhibiting or promoting plant cell growth. The method involves the use of chimeric gene constructs to achieve expression of SAG, in the case of promoting growth of plants, or anti-sense SAG, in the case of inhibiting plants (i.e., weeds), polynucleotide sequences in selected target plant cells.

The dosage regimen for *in vivo* oxygen radical scavenging by the administration of SAG protein is based on a variety of factors, including the type of injury, the age, weight, sex, medical condition of the individual, the severity of the condition, the route of administration, and the particular compound employed. Thus, the dosage regimen may vary widely, but can be determined routinely using standard methods. In a preferred embodiment, the pharmaceutical composition comprises between 0.1 and 100 mg of SAG protein. In a most preferred embodiment, the pharmaceutical composition comprises between 1 and 10 mg of SAG protein.

The SAG protein may be made up in a solid form (including granules, powders or suppositories) or in a liquid form (*e.g.*, solutions, suspensions, or emulsions). The SAG protein may be subjected to conventional pharmaceutical operations such as sterilization and/or may contain conventional adjuvants, such as preservatives, stabilizers, wetting agents, emulsifiers, buffers etc.

While the SAG protein can be administered as the sole active pharmaceutical agent, they can also be used in combination with one or more other agents. When administered as a

combination, the therapeutic agents can be formulated as separate compositions that are given at the same time or different times, or the therapeutic agents can be given as a single composition.

For administration, the SAG protein is ordinarily combined with one or more adjuvants appropriate for the indicated route of administration. The SAG protein may be admixed with lactose, sucrose, starch powder, cellulose esters of alkanoic acids, stearic acid, talc, magnesium stearate, magnesium oxide, sodium and calcium salts of phosphoric and sulphuric acids, acacia, gelatin, sodium alginate, polyvinylpyrrolidine, and/or polyvinyl alcohol, and tableted or encapsulated for conventional administration. Alternatively, the SAG protein may be dissolved in saline, water, polyethylene glycol, propylene glycol, carboxymethyl cellulose colloidal solutions, ethanol, corn oil, peanut oil, cottonseed oil, sesame oil, tragacanth gum, and/or various buffers. Other adjuvants and modes of administration are well known in the pharmaceutical art. The carrier or diluent may include time delay material, such as glyceryl monostearate or glyceryl distearate alone or with a wax, or other materials well known in the art.

In a preferred embodiment of the present invention, the SAG protein pharmaceutical composition is administered intramuscularly (IM) or intravenously (IV). A suitable IM or IV dose of active ingredient of SAG protein is 5 mg/mL administered daily. For IM or IV administration, the active ingredient may comprise from 0.001% to 10% w/w, *e.g.*, from 1% to 2% by weight of the formulation, although it may comprise as much as 10% w/w, but preferably not more than 5% w/w, and more preferably from 0.1% to 1% of the formulation.

The present invention may be better understood with reference to the accompanying examples that are intended for purposes of illustration only and should not be construed to limit the scope of the invention, as defined by the claims appended hereto.

Examples

Example 1. Identification of an OP-inducible gene

The differential display (DD) technique was employed to isolate genes responsible for or associated with OP-induced apoptosis in two murine tumor lines. Since OP induced-apoptosis can be visually detected at 12 hours post exposure (Sun, (1997) FEBS Lett. 408:16-20), it was reasoned that gene(s) responsible for apoptosis induction should be up- or down-regulated prior to the appearance of apoptosis. Six hours of OP treatment was conducted, therefore, in one of these tumor lines followed by the DD analysis.

Mouse JB6 tumor line L-RT101 (an epidermal originated tumor cell line) was cultured in Minimal Essential Medium with Earle's salts (BRL) containing 5% fetal calf serum (Sigma). H-Tx cells, a spontaneously transformed mouse liver line, were cultured in Dulbecco's Modified Eagle Medium containing 10% fetal calf serum and 1 mM sodium pyruvate. Human colon carcinoma line DLD-1 was grown in 10% DMEM.

L-RT101 cells were treated with 150 uM OP for 6 hours and subjected to differential display analysis using DMSO-treated cells as a control. Briefly, total RNA was isolated from both OP-treated and control cells using RNAzol solution (Tel-Test) according to the manufacturer's instructions, and subjected to reverse transcription (RT), performed as previously described (Sun et al. (1993) Mol. Carcinogenesis 8, 49-57), followed by the polymerase chain reaction (PCR). The primer used for reverse transcription (P1) consisted of the sequence 5 AAGCTTTTTTTTTTTTR (**SEQ ID 5**), wherein R consists of either adenine, guanine or cytosine. P1 was used as the downstream primer in the subsequent PCR while the upstream primer consisted of the sequence AAGCTTNNNNNNN (**SEQ ID 6**), wherein N consists of adenine, cytosine, guanine, or thymine.

Primers P1 and P2 reproducibly detected differential expression between the control and OP-treated cells. The fragments reproducibly showing differential expression were PCR amplified using the same primers and used as probes for Northern analysis (Sun et al. (1992) Cancer Res. 52:1907-1915) of both L-RT101 and H-Tx cells treated with OP (Sun (1997) FEBS Letters 408:16-20). Those fragments that were induced by OP (as determined by Northern analysis) were then subcloned into TA cloning vectors (In Vitrogen) according to the manufacturer's instructions, and sequenced by DNA Sequenase Version 2.0, according to the manufacturer's instructions (Amersham). The resulting clones comprise OP-inducible cDNA fragments.

Example 2. cDNA library screening and 5'RACE

One of the OP-inducible clones was used as a probe to screen a mouse lung cDNA library to clone the full length mouse SAG cDNA. Briefly, 1 x 10^6 recombinant plaques were plated onto 1% NZY in 150 mm plates (a total of 20). The recombinant phage DNA was transferred to nitrocellulose membrane and hybridized with mouse SAG probe ($2X10^8$ cpm/μg) in a hybridization solution containing 5X SSC, 5X Denhardt solution, 50 mM sodium phosphate, and 100 μg/mL denatured DNA at 60°C for 16-18 hours. The filter was

then washed once for 5 min in a solution of 2XSSC/0.1% SDS, once for 5 min in 0.5XSSC/0.1% SDS, and twice 0.1XSSC/0.1% SDS for 15 min.

The longest clone isolated was a 1.0 kilobase ("kb") fragment consisting of a partial open reading frame and the entire 3'-end untranslated region. A mouse brain Marathon-Ready cDNA (ClonTech) was screened via PCR amplification using a primer derived from the 1 kb fragment and another primer derived from the vector sequence, according to the protocol supplied with the cDNA library. This yielded a further 100 bp fragment consisting of 5'-end untranslated sequence and some of the coding sequence. The derived cDNA clone consists of 1140 base pairs ("bp") (SEQ ID 1) that encode a novel deduced protein of 113 amino acids, containing 12 cysteine residues (SEQ ID 2). The open reading frame was preceded by 17 bp upstream sequence. The start codon was located in a context that conformed 100% to the Kozak consensus sequence (Kozak,M. (1991) J. Biol. Chem. 266, 19867-19870). An in-frame stop codon was identified 72 bp upstream of the start codon in the 5' untranslated region in one genomic clone (not shown). The 3'-end untranslated region consists of 792 bp sequence with two polyadenylation signals (AATAAA). These data indicate that a near full length cDNA was isolated.

The mouse cDNA was used as a probe to screen a human HeLa cell cDNA library (Strategene) as described above. One positive clone was isolated and purified through two more cycle of screening. In this manner, a 754 bp clone containing a polyadenylation signal at the 3' end was isolated (SEQ ID 3). The human cDNA also contains an open reading frame encoding a novel predicted 113 amino acid polypeptide containing 12 cysteine residues (SEQ ID 4). The sequence identity between the isolated mouse and human cDNAs is 82% in overall sequence and 94% in the coding region. At the protein level, they shared 96.5% identity, with all 12 cysteine residues being conserved. Computer analysis of protein databases using the GCG program (Genetics Computing Group, Madison, WI) revealed that the encoded proteins share 70% identity with hypothetical proteins from yeast (accession #Z74876) and C-elegans (accession #80449).

Motif searching of the deduced protein sequences using the GCG program did not reveal any known functional domains. However, they each contain two imperfect heme binding sites (CXXCH, at codons 47-51 and 50-54) (Matthews, Prog. Biophys. Mol. Biol. 45:1-56, 1985) and one imperfect C_3HC_4 zinc ring finger domain (Freemont et al., Cell 64:483-484, 1991) at the C-terminal of the molecule (Fig. 1A) among other consensus motifs. The second potential heme binding domain (Fig. 1A) contains a substitution of arginine to

histidine (amino acid 54). Since these two amino acids are structurally similar, this may constitute an authentic heme binding site. The zinc ring finger domain mismatch involves substitution of cysteine by histidine at amino acid 85. The ring finger domain in this protein is a $C_3H_2C_3$ structure, rather than the consensus C_3HC_4 structure. Since cysteine and histidine residues are interchangeable in zinc binding (Berg and Shi, Science 271:1081, 1996; Inouye et al., Science 278:103-106, 1997), the $C_3H_2C_3$ domain in these proteins may comprise authentic zinc-binding sites. Significantly, these heme and zinc ring finger domains are 100% conserved among *C. elegans*, mouse and human. In yeast, only the last cysteine residue in $C_3H_2C_3$ motif was not conserved. This evolutionary conservation of the heme and zinc-binding domains suggest their functional importance.

Other motifs identified in the deduced sequence of the SAG protein, when allowing for a single mismatch, include an aminoacyl-transfer RNA synthetase class II motif (codons 54-63), a Kazal serine protease inhibitor family motif (codons 85-107), a Ly-6/U-par domain (codons 65-107), a prokaryotic membrane lipoprotein lipid attachment site (codons 16-27), and somatotropin, prolactin and related hormone motifs (codons 49-66).

These experiments thus resulted in the cloning of novel mouse and human genes that encode nearly identical, evolutionarily conserved protein that contain distinct heme and zinc binding motifs.

Example 3. SAG is inducible by OP in both mouse and human tumor cells

To confirm that the cloned cDNAs are subject to OP induction, a Northern analysis was performed with RNAs isolated from mouse tumor lines L-RT101 and H-Tx, and human colon carcinoma line DLD-1. Subconfluent cells were treated with 150 μM OP for various times up to 24 hours and subjected to total RNA isolation. Fifteen μg of total RNA was subjected to Northern analysis using mouse SAG or human SAG cDNA as probes.

Both cloned mouse and human cDNAs detected an OP inducible transcript with a size of 1.2 kb and 0.9 kb, respectively. Since these genes were induced in the OP-induced apoptosis pathway, the genes were named Sensitive to Apoptosis Genes (hereinafter referred to as "SAG"), which encode SAG proteins.

Example 4. Tissue distribution and embryonic expression of SAG

SAG expression was next examined in multiple human tissues. The assays were performed as detailed previously (Sun et al. (1993) Mol. Carcinogenesis 8, 49-57; Sun et al., Proc. Natl. Acad. Sci. USA 90:2827-2831, 1993). Briefly, total RNA was isolated from

multiple human tissues (ClonTech) and then subjected to Northern blot analysis using the mouse or human SAG cDNA as probes. SAG RNA was detected in all tissue examined including heart, brain, pancreas, lung, liver, skeletal muscle, kidney, pancreas, spleen, thymus, prostate, testis, ovary, small intestine, colon, and peripheral blood leukocytes. A very high expression level was detected in heart, skeleton muscle and testis, which consume high levels of oxygen. Its tissue distribution and high level expression in oxygen-consuming tissues, and its induction by a redox sensitive compound (OP), implies that SAG encodes a redox sensitive protein.

Since SAG protein is evolutionarily conserved, the possible developmental role of SAG was tested by measuring SAG expression in mouse embryonic tissue (provided by Dr. Tom Glaser, University of Michigan), using reverse transcription of total RNA followed by PCR with the following primers: SAGTA.01 5′-CGGGATCCCCATGGCCGACGTGAGG-3′ (**SEQ ID 7**) and SAGT.02 5′-CGGGATCCTCATTTGCCGATTCTTTG-3′ (**SEQ ID 8**), which flank the entire SAG coding region. The PCR reaction mixture for 11 samples contained 55 µL of 10X buffer, 22 µL of 1.25 mM dNTP, 1.1 µL of SAGTA.01 and SAGT.02, respectively, 5.5 µL of Taq DNA polymerase, 5.5 µL of ^{32}P-dCTP and sterile water up to 495 µl. Into each tube which contains 5 µL of first strand cDNA reverse-transcribed for total RNA isolated from mouse embryonic tissues (Sun et al. (1997), Mol. Carcinogenesis 8:49-57), 45 µL of reaction mixture was added and PCR was performed for 25 cycles (95°C for 45 sec, 60°C for 1 min and 72°C for 2 min). A 5 µL aliquot of the PCR product was denatured and separated on a sequencing gel, which was dried and exposed to X-ray film.

SAG RNA was expressed in 9.5 day old to 19.5 day old whole mouse embryos, with a higher level of expression detected between days 9.5 and 11.5. These results suggest that SAG plays a role in embryonic development.

Example 5. Cellular localization by immunofluorescence

NIH3T3 cells (ATCC CRL 1658) were plated on coverslips in 24-well culture dishes and transfected by the calcium phosphate method according to standard techniques (Sambrook et al, 1989) with the following constructs: pcDNA3.1 (Invitrogen vector pcDNA 3 with a myc-his-tag); pcDNA3.1-SAG (human SAG cDNA subcloned into the BamHI site of pcDNA3.1, downstream from the CMV promoter and upstream and in-frame with the myc-his-tag, such that upon expression, the resulting fusion protein consists of the SAG

protein followed by the myc-his tag at the carboxy-end of SAG); or pcDNA3.1-LacZ (Invitrogen). Two days post-transfection, cells were washed once with cold PBS and then fixed with 3% formaldehyde in PBS for 10 minutes followed by 5 minutes in 1:1 methanol:acetone. The fixed cells were washed 4 times in PBS and incubated with antibody directed against the Myc-tag (Invitrogen 1:200 dilution) in PBS containing 1% BSA, 0.1% saponin, 2 µg/mL DAPI for 1 hour in the dark with shaking. Cells were then washed 4 times with 0.1% saponin in PBS and incubated with FITC-conjugated goat anti-mouse antibody (Jackson Laboratory, 1:100 dilution) for 1 hour in the same conditions as the first antibody. After incubation cells were washed 4 times with 0.1% saponin in PBS and twice with PBS. The coverslips were then mounted to glass slides with non-fade mounting medium and analyzed using a Leita Dialux 20 microscope.

SAG fusion protein was detected in both the cytoplasm and nucleus, while the β-galactosidase control was expressed predominately in the cytoplasm. No immunofluorescence staining was detected with the vector-only control. The cytoplasmic/ nuclear localization of SAG was confirmed also in a SAG stable transfectant using both SAG and myc-tag antibodies. These data demonstrate that exogenously expressed SAG fusion proteins can be detected within transfected cells by using antibodies directed against an epitope fused to SAG protein.

Example 6. Expression and purification of SAG protein in bacteria

The entire open reading frame of the human SAG cDNA was PCR amplified as described above and subcloned into the pET11 expression vector (Novogen) under control of the T7 promoter, yielding construct pET11a-hSAG. The sequence and orientation of the SAG DNA insert were confirmed by DNA sequencing. pET11a-hSAG was used to transform *E. coli* strain BL21 (Novagen, Inc.). Transformed cells were grown in LB media containing ampicillin (50 µg/mL). SAG expression was induced by 0.5 mM IPTG and SAG protein was found in inclusion bodies, which were subsequently isolated as follows.

Following IPTG induction, four liters of cells were grown for 4.5 hours at 37°C at a shaker setting of 150 rpm. Cell pellets were obtained by centrifugation at 5000 rpm for 10 minutes, and were resuspended in 100 mL TN buffer (20 mM Tris-HCl, pH 7.5, 50 mM NaCl) containing 100 µM PMSF. The resuspended cell pellet was subsequently sonicated (15 sec/round for 5 rounds at a setting of 15 on Model 50 sonic dismembrator, Fisher Scientific) and subjected to pressure of 2500 pounds/square inch on a French cell press,

followed by addition of 1 mM MgCl2 and 10 mg of DNase I. The cell lysate was placed on ice for 30-60 minutes and then centrifuged at 18,000 rpm and the supernatant was disposed.

The pellet was seen to have 2 layers. The white layer on the top was carefully blown loose with TN buffer and removed. The remaining dark brown layer on the bottom was resuspended thoroughly in 15 mL of urea buffer (7 M urea, 20 mM Tris-HCl, pH 7.5, 200 mM NaCl) and allowed to sit overnight at room temperature. The resuspended cell pellet was vigorously homogneized with a serological pipette and then centrifuged at 40,000 rpm for 40 minutes using an SW50 ultracentrifuge rotor. The supernatant was collected and concentrated using a Centricon-10 concentrator to a volume of 5 mL and loaded onto a Sephacryl-100 column (100 cm long with a diameter of 2.5 cm) that had been equilibrated with urea buffer. The column was run at a rate of 0.25 mL/min and fractions were collected. The early fractions containing a brownish color consisted of mostly the large molecular weight protein, as expected. They also contained a protein with the same size of SAG protein (approximately 13 kDa). Since SAG protein contains 12 cysteine residues, it follows that SAG protein may form oligomers when expressed in bacteria and thus may elute as a SAG protein oligomer. Since SAG is a redox-sensitive protein, the DTT present in SDS sample buffer reduces SAG protein oligomers to monomer, leading to the detection of a fast migrating band. When early fractions were run in SDS-PAGE without DTT, the 13 kDa SAG protein band disappeared, and a 260 kDa band was detected, representing a SAG protein 20-mer. This unique feature helped us to purify SAG protein. Early fractions were pooled and loaded on the same Sephacryl-100 column pre-equilibrated with 7M urea and 5mM DTT.

SAG protein oligomer was reduced to monomer by using DTT in the loading buffer and was eluted in the later fractions, thus separating it from high molecular weight contaminant proteins (eluted earlier). The brownish fractions were pooled and concentrated using a Centricon-10 to a volume of 5 mL. DTT was added to a concentration of 5 mM. The combined fractions were loaded onto an S-100 column (100 cm long with a diameter of 2.5 cm), that had been equilibrated with urea buffer plus 5 mM DTT. The column was run at a rate of 0.25 mL/min and fractions were collected. The fractions containing SAG protein are brownish in color, highly suggesting that SAG is a heme-containing protein. The SAG protein containing fractions and their sensitivity to DTT were confirmed by Western blot using SAG antibody. The brownish fractions were pooled and concentrated using a Centricon-10 concentrator to a volume of 2 mL. The resulting sample was dialyzed against 4 liters of dialysis buffer (150 mM KCl, 20 mM Tris-HCl, pH 7.5) at 4°C overnight to

remove urea and DTT to yield refolded SAG protein. The dialyzed sample was loaded onto an S-100 column (100 cm long with a diameter of 2.5 cm), that had been equilibrated with dialysis buffer. The brownish fractions were pooled and concentrated using a Centricon-10 to a volume of 1 mL. The resulting sample was stored at 4°C. The protein concentration was determined by a BioRad protein assay. The purity of the samples was demonstrated in 10-20% SDS-PAGE. These data demonstrate the purification of recombinant SAG protein.

Example 7. Redox Sensitivity of SAG Protein

To confirm that purified recombinant SAG protein possesses the same redox sensitivity as it shows during protein purification, the sensitivity of refolded SAG to redox reagents was examined next. SAG protein (1 μg) was exposed to various concentrations of DTT (1 M, 300 mM, 100 mM, or 30 mM) or H_2O_2 (15 mM, 50 mM, 150 mM or 450 mM) for 10 min before being separated by polyacrylamide gel electrophoresis (PAGE), followed by Western blot analysis. Alternatively, 10 μg of SAG protein was incubated with 50 mM H_2O_2 for 10, 30, 60 or 120 minutes followed by PAGE separation and Coomassie Blue staining.

Dimers of SAG protein are rather resistant to reducing reagent DTT since no significant dimer was reduced to monomer after DTT treatment. However, as little as 15 mM H_2O_2 induces oligomerization of SAG protein, possibly through the formation of intermolecular disulfide bonds. The oligomerization is incubation-time dependent, as higher order SAG protein oligomers were detected upon increased incubation time. Interestingly, a band migrating faster than the monomer form is observed upon H_2O_2 treatment, and the monomer form of SAG protein becomes a doublet, possibly due to the formation of intramolecular disulfide bonds.

In order to determine whether H_2O_2-induced SAG protein oligomerization can be reversed by DTT treatment, 1 μg of purified SAG protein was incubated with 50 mM H_2O_2 for 10 minutes, followed by a 10 minute incubation with either H_2O_2, 50 mM DTT, 100 mM, 500 mM, or 1 M DTT. The samples were separated via PAGE followed by Western analysis. The results demonstrated that H_2O_2-induced SAG protein oligomerization can be reversed by subsequent incubation with DTT in a dose dependent manner, indicating that SAG protein oligomerization is subject to redox regulation.

To confirm that SAG protein oligomerization and doublet formation is due to inter- and intra-molecular disulfide bond formation, respectively, SAG protein was treated, prior to H_2O_2 exposure, with 50 mM N-ethylmaleimide (NEM), an alkylating reagent that will alkylate the free SH-groups in SAG protein. Purified SAG protein (1 μg) was pre-incubated with 50 mM NEM or DMSO, or buffer only, for 10 minutes prior to H_2O_2 treatment. The samples were separated via PAGE, followed by Western blot analysis. Pre-incubation of SAG protein with DMSO did not affect H_2O_2-induced oligomerization and doublet formation, whereas NEM pre-treatment abolished H_2O_2 activity. Neither inter- (oligomerization) nor intra- (doublet monomer) disulfide bonds were formed, demonstrating that alkylation of the free SAG protein SH groups abolishes H_2O_2 sensitivity. These data demonstrate that SAG protein is redox sensitive. It is subjected to both intra- and inter-molecular disulfide bond formation upon exposure to H_2O_2, as evidenced by both doublet and oligomer formation. These H_2O_2-induced changes can be reversed by subsequent treatment with reducing reagents, including DTT, or can be prevented by NEM pretreatment. It has also been observed that zinc can promote H_2O_2-induced oligomerization, although zinc itself did not induce oligomerization.

Example 8: Production of SAG mutants

In order to understand the role of each particular cysteine residues in heme binding and SAG oligomerization, a series of single and double SAG mutants were made in heme binding sites as well as the zinc ring finger motif (see Figure 1B). To generate single point mutations in SAG cDNA, 15 pairs of sense and antisense primers were designed, which are partially complimentary and contain a desired point mutation. The wildtype SAG cDNA cloned into the pET11a vector at the Nhe I/Bam HI sites was used as the template for PCR amplification. Two separate PCR reactions were conducted using a) primer SAG P.01 (5′-TATGGCTAGC ATGGCCGACGTGGAGG-3) (**SEQ ID 9**) and each of antisense primers and b) each of sense primers and SAG T.02 (**SEQ ID 8**), respectively. The resultant PCR products that overlap with each other and contain a desired point mutation were mixed and served as templates for a third PCR. The primers used were SAG P.01 and SAG T.02, which flank the entire encoding region of SAG cDNA. The PCR was performed as previously described (Sun et al. (1992) BioTechniques 12:639-640). The PCR products were digested with restriction enzymes Nhe I and Bam HI and subcloned into the pET11a vector, which was digested with the same restriction enzymes. To generate SAG double mutants

(MM10, MM13, MM14, see Figure 1B), a QuickChange site-directed mutagenesis kit was purchased from Strategene (La Jolla, CA) and used as instructed. All SAG mutants generated were verified by DNA sequencing (SEQ ID 21, SEQ ID 23, SEQ ID 25, SEQ ID 27, SEQ ID 29, SEQ ID 31, SEQ ID 33, SEQ ID 35, SEQ ID 37, SEQ ID 39, SEQ ID 41, SEQ ID 43, SEQ ID 45, SEQ ID 47 and SEQ ID 49). The predicted mutant SAG proteins encoded by these mutant SAGs are shown in SEQ ID 22, SEQ ID 24, SEQ ID 26, SEQ ID 28, SEQ ID 30, SEQ ID 32, SEQ ID 34, SEQ ID 36, SEQ ID 38, SEQ ID 40, SEQ ID 42, SEQ ID 44, SEQ ID 46, SEQ ID 48, and SEQ ID 50.

Individual SAG mutant-expressing vectors were used to transform *E.coli* strain BL21 (Novagen, Inc.). Mutant SAG protein was expressed and purified as detailed in Example 6. The fractions after a Sephacryl-100 column were collected and analyzed on 8-25% Phast gels followed by Coomassie blue protein staining. The pure fraction containing mutant SAG protein was dialyzed in 4 liters of 20 mM Tris-HCl, pH 7.5 and used for SAG protein oligomerization studies.

Purified wildtype SAG protein is a heme-containing brownish protein (See Example 9). Some of the purified SAG protein mutants were found to have either lost the brownish color (MM3 and MM13) or had decreased brownish color (MM1) compared to wildtype SAG protein. This color change indicates the loss or decrease of heme binding (Table 1).

TABLE 1. SUMMARY OF SAG MUTANTS

NAME	*MUTATION SITE(S)*	*HEME BINDING*	*OLIGOMERIZATION*
WT	None	+++	Yes
MM1	C_A/heme	++	Yes
MM2	C_B/heme	+++	Yes
MM3	C_{A+B}/heme	+/-	Yes
MM4	C_1/Zn-ring finger 1	+++	Yes
MM5	C_3/Zn-ring finger 1	+++	Yes
MM6	H_4/Zn-ring finger 1	+++	Yes
MM7	H_5/Zn-ring finger 2	+++	Yes
MM8	C_6/Zn-ring finger 2	+++	Yes
MM9	C_7/Zn-ring finger 2	+++	Yes
MM10	H_{4+5}/Zn-ring fingers 1&2	+++	Yes
MM11	C_2/Zn-ring finger 1	+++	Yes
MM12	C_c/protease inhibitor	+++	Yes
MM13	C_{1+2}/Zn-ring finger 1	+/-	Yes
MM14	C_{7+8}/Zn-ring finger 2	+++	No
MM15	GADPH binding site	+++	Yes

To examine mutant SAG protein oligomerization, each mutant SAG protein as well as wildtype SAG was treated with 50 mM H_2O_2 for 10 min. All of the SAG mutants, except MM14, can be oligomerized upon exposure to H_2O_2. The mutant 14, which is a double mutants in positions of C7 and C8 in the zinc ring finger domain, becomes insensitive to oligomerization (Table 1), indicating that these two positions are important for intermolecular disulfide bond formation.

Example 9. Heme measurement of SAG protein

Heme content in SAG protein was measured as previously described (Rieske (1967) Methods in Enzymol. 76, 488-493). Briefly, 1 mg of purified SAG protein, along with cytochrome C, catalase, and BSA as controls, was extracted with cold acetone (0.5 mLs)

After centrifugation the pellet was extracted sequentially with 0.5 mL of chloroform:methanol (2:1); 0.5 mL of cold acetone, and finally 0.5 mL of cold acetone containing 5 μL of 2.4 N HCl. The acetone extracts were dried under speed-vac and dissolved in 0.5 mL of pyridine. After addition of 0.5 mL of 0.2 N NaOH, the solution was centrifuged briefly and clear supernatant was recovered. One drop of diluted potassium ferricyanide (0.05 M) was added to the supernatant and the absorbance was read at 556 nm in 1.0 mL quartz cuvettes using water as a blank. The solution was then reduced by adding 10 uL of 2 M DTT and absorbance was read at 556 nm, 587 nm and 550 nm, respectively.

Heme absorbance at 556, 587, and 550 nm was observed in SAG protein, as well as in cytochrome C and catalase, but not in BSA. This result demonstrated that SAG protein contains heme, but did not reveal the molar ratio between SAG protein and heme molecule.

Example 10. SAG protein antibody production

Two polyclonal antibodies against SAG protein were generated using standard methods [by Zymed Laboratories, Inc. (San Francisco) under a service agreement with Warner-Lambert]. Briefly, the peptide antibody was generated as following. A 16-amino-acid peptide (SAG-Pep1: QNNRCPLCQQDWVVQR) (**SEQ ID 10**) located in the C terminus of SAG protein (codons 95-110) was synthesized and purified via standard techniques. The purified peptide was conjugated to keyhole limpet hemocyanin (KLH) via cysteine residues. The conjugated peptide (0.5 mg) was emulsified with equal volume of Complete Freund Adjuvant (CFA) and subcutaneously injected into rabbit, followed by 4 boosts with 0.5 mg each in Incomplete Freund Adjuvant (IFA) at 3 week intervals. Rabbits were bled 10 days after the final boost and antiserum was collected. The same protocol was used for protein antibody production using purified human SAG protein as the antigen, prepared as described above.

Example 11. Analysis of SAG protein transcriptional regulatory activity

SAG protein belongs to the zinc ring finger protein families by virtue of its $C_3H_2C_3$ motif (Saurin et al. (1996) TIBS 21, 208-214). Some zinc ring finger proteins have been shown to bind to DNA and function as transcriptional repressors (for example, RING1) (Satijn et al. (1997) Mol. Cell. Biol. 17, 4105-4113), whereas others function as transcriptional activators (Chapman and Verma (1996) Nature 382, 678-679; Monteiro et al. (1996) Proc. Natl. Acad. Sci. USA 93, 13595-13599). To examine the transcriptional regulatory activity of SAG protein, the cDNA encoding the entire open reading frame of

human SAG was PCR amplified and fused both in frame and as an antisense fusion, downstream of the Gal-4 DNA binding domain (encoding amino acids 1-147) in the pG4 vector (Sadowski et al., Nature 335:563-564, 1988). The resulting construct was sequenced to confirm in frame fusion and freedom from PCR-generated mutation. The construct was co-transfected along with a chloramphenicol acetyltransferase (CAT)-reporter-expressing vector (Sadowski et al., Nature 335:563-564, 1988) as well as a β-galactosidase reporter whose expression is driven by a CMV promoter for normalization of transfection efficiency into human kidney 293 cells (ATCC accession number CRL1573) by the calcium phosphate method. CAT activity was measured 36 hours post-transfection using a CAT assay kit (Quan-T-CAT; Amersham) according to the manufacturer's instructions. PG4-VP16, a known transcription factor (Triezenberg et al., Genes and Develop. 2:718-729, 1988), fused downstream of the Gal4 DNA binding domain was used as a positive control. Activation was calculated by arbitrarily choosing CAT activity from the vector control as 1 and comparing the other constructs to it. Three independent transfections and assays were performed.

SAG protein showed no transactivation activity. The positive control, VP16 showed 300-fold activation of CAT activity. To test for transrepression activity, SAG constructs (both sense and antisense) were co-transfected with pG4-VP16. Again, neither orientation of SAG induced significant expression of VP16-induced transactivation. These results demonstrated that SAG protein lacks transcriptional regulatory activity when fused downstream Gal-4 DNA binding domain.

Example 12. SAG is an RNA binding protein

The zinc-ring finger domain of the MDM2 protein has been shown to bind to RNA (Elenbaas et al. (1996) Mol. Med. 2, 439-445). Since SAG protein showed no transcriptional regulatory activity, it was tested whether SAG protein could bind to RNA or DNA. Binding of purified SAG protein to different nucleic acid cellulose conjugates was performed as described (Elenbaas et al. (1996)). Briefly, 0.5 μg of SAG protein was incubated in 300 μL RNA binding buffer for 1 hour at 4°C with double-stranded calf thymus DNA, denatured calf thymus DNA (ssDNA), or one of 4 RNA homopolymer columns (Sigma) conjugated to agarose or cellulose beads (Sigma), and used according to the manufacturer's instructions. RNA binding buffer consisted of 20 mM Tris, pH 7.5, 150 mM NaCl, 5 mM $MgCl_2$, 0.1% nonidet P-40, 50 μM $ZnCl_2$, 2% glycerol, and 1 mM DTT. The columns were washed with 3 mL RNA binding buffer to remove non-specifically bound protein from the beads, which

were then boiled in SDS sample buffer. The protein so eluted from the beads was separated by SDS-PAGE, transferred to nitrocellulose for Western blot analysis using the polyclonal antibody directed against SAG protein described previously detected by ECL chemiluminescence (Amersham) according to the manufacturer's instructions.

Purified SAG bound to polyU, polyA, and polyC RNA, respectively. No binding was seen with polyG RNA or ssDNA. A band showing dsDNA binding did not agree with SAG molecular weigh. Oligomeric SAG protein bound to polyU RNA, whereas the monomeric form of SAG binds to polyA and polyC RNA. Purified SAG protein was run as a marker. These results suggest that SAG is an RNA binding protein and that binding specificity is determined by the oligomeric form of SAG protein.

Example 13. Identification of two deletion mutants of SAG in cancer cell lines

Total RNA was isolated from DLD-1 colon carcinoma cells (ATCC accession number CCL221) and subjected to RT-PCR using primers SAG TA.01 and SAG T.02. The resulting PCR fragments were subcloned into the TA cloning vector (Invitrogen). During sequence verification of the resulting clones, it was found that several clones contained either a 7 bp or a 48 bp deletion at nucleotide 170 or 177, respectively, assigning the first A at the start codon as nucleotide #1. Both SAG deletions encode the potential heme-binding sites. The 7 base pair deletion (SAG mutant 1) **(SEQ ID 11)** is a frame shift deletion that abolishes the downstream encoded zinc-ring finger motif in the resulting protein **(SEQ ID 12)**, whereas the 48 base pair deletion (SAG mutant 2) **(SEQ ID 13)** is an in-frame deletion that eliminates 16 amino acids in the encoded protein **(SEQ ID 14)**, but retains the zinc-ring finger motif.

Total RNA was isolated from a total of 20 human tumor lines and transformed lines originating from lung, brain, kidney, prostate, testis, nasopharynx, bone, cervix and foreskin and subjected to RT-PCR analysis as described previously (Sun et al. (1993) Mol. Carcinogenesis 8, 49-57). Genomic DNA was also isolated from these cell lines and subjected to PCR amplification as described (Sun et al. (1992) BioTechniques 12:639-640). The primers used for PCR were hSAG.M1, 5′ GCCATCTGCAGGGTCCAG-3′ **(SEQ ID 15)**, starting at nt 151 of hSAG cDNA, and SAGT.02-1 5′–GGATCCTCATTTGCCGATTCTTTGGAC-3′ **(SEQ ID 16)**, including stop codon (underlined). The resulting fragment is 200 bp for wildtype SAG. The PCR was conducted in the presence of ^{35}S-dATP (Amersham) and PCR products were resolved in 6% denaturing sequencing gels, as described previously (Sun et al. (1995) Cancer Epidemiology, Biomarkers & Prevention, 4, 261-267). The bands corresponding to wildtype as well as the

two deletion mutants were cut out from the gel, PCR amplified using the same set of primers, and sequenced to verify the DNA sequence of the resulting PCR fragments.

Both the 7 base pair and the 48 base pair deletions were detected in RNA from only the CATES-1B cell line, a testicular carcinoma line obtained from ATCC (accession number HTB104). This tumor line also contains the wildtype SAG DNA sequence. The identity of these three bands was confirmed by DNA sequencing after PCR amplification and TA cloning. HONE-1, a nasopharyngeal carcinoma line which only contains wildtype SAG was included for comparison.

It was next examined whether these SAG deletions were detectable at the DNA level. Genomic DNA was isolated from CATES-1B cells and subjected to PCR analysis, as described previously (Sun et al. (1992) BioTechniques 12:639-640). The primers used were hSAG.M1 and SAG T.02 (see above for sequences). Genomic DNA from CATES-1B cells possesses only wildtype SAG and no SAG deletion mutants were detected. These results indicate that the SAG deletion mutations occur very rarely in human cancer lines. Detection of the mutations in SAG RNA, but not genomic DNA, may reflect an RNA editing modification of SAG messenger RNA.

Example 14. Production of stable SAG transfected mammalian cells

The potential biological function of human SAG protein was examined next by its overexpression in cells. DLD-1 cells were transfected with the following plasmids: the neo control pcDNA-3 (Invitrogen) (identical to pcDNA3.1 described above, except that it lacks the myc-his tag), pcDNA-SAG, pcDNA-SAG-mutant-1, and pcDNA-SAG-mutant-2 (pcDNA3 with SAG, SAG 1 or SAG 2 subcloned into the BamHI site, respectively, using methods well known in the art). The SAG mutant constructs were generated by RT-PCR as follows. Total RNA was isolated from DLD-1 cells, and subjected to reverse transcription, followed by PCR amplification. The primers used were SAG.TA01 (**SEQ ID 7**) and SAGT.02 (**SEQ ID 8**), which flank the entire coding region of SAG gene. The PCR products were digested with restriction enzyme Bam HI, and subcloned into pcDNA3 (In Vitrogen, San Diego), a mammalian expression vector under the transcriptional control of the CMV promoter, which drives gene expression constitutively. The resultant clones were sequenced to confirm both sense and antisense orientation and freedom of PCR-generated mutations. DNA sequencing revealed wildtype SAG clone as well as two deletion mutants: SAG-mutant-1 (7 bp deletion, SEQ ID 11) and SAG-mutant-2 (48 bp deletion, SEQ ID 13) in DLD-1 tumor cells.

DLD-1 cells were transfected by lipofectamine (BRL) with plasmids expressing wildtype (both sense and antisense orientation), SAG mutant-1, and SAG mutant-2, along with the neo control vector. Neomycin resistant colonies were identified by G418 selection (600 μg/mL) for 18 days. Stable clones were ring-isolated by well known methods (Sun et al. (1993) Proc. Natl. Acad. Sci. USA. 90: 2827-2831) and SAG expression was monitored by Northern analysis. Selected clones were examined for SAG protein expression by immunoprecipitation, as described below.

Total RNA was isolated from the cloned cell lines and subjected to Northern analysis. Cell lines transfected with the following constructs were analyzed: vector controls D1-3 and D1-6; SAG-wildtype D12-1 and D12-8; SAG-mutant-1 D3-3 and D3-4; and SAG-mutant-2 D4-2 and D4-5.

Northern blot analysis of RNA from selected stable SAG-expressing clones probed with the human SAG cDNA demonstrated that all SAG transfectants express SAG mRNA, while very low levels of endogenous SAG message were detected in the neo control cells.

The vector control lines and SAG wildtype and SAG deletion mutant transfectants were subsequently subjected to immunoprecipitation using standard techniques (Sun et al. (1993) Proc. Natl. Acad. Sci. USA. 90: 2827-2831, Sun et al. (1993) Mol. Carcinogenesis 8, 49-57). Subconfluent SAG transfectants were subjected to methionine starvation for 1 hour and then metabolically labeled with ^{35}S-translabel (0.2 mCi/mL) for 3 hours. Cells were then lysed on ice for 30 minutes in a lysis buffer comprising 2% Nonidet P40, 0.2% SDS, 0.5% sodium deoxycholate, 1 mM sodium orthovanadate, 5 mM sodium fluoride, 5 mM sodium pyrophosphate, 1 mM phenylmethylsulfonyl fluoride, and 1 μl/mL leupeptin, and centrifuged at 12,000 x g. The TCA precipitable radioactivity in the supernatant (1 x 10^8 cpm) was immunoprecipitated using rabbit anti-human SAG antibody (generated as described above). The immunoprecipitates were collected, washed, and analyzed on a 10-20% SDS-polyacrylamide gel, followed by autoradiography. High SAG protein expression was detected only in the wildtype transfectants. The antibody used did not recognize the two SAG protein mutants. These data demonstrate the production of stably transfected cells expressing either wildtype or mutant SAG protein

Example 15. Morphological appearance of SAG transfectants after exposure to redox reagents

Two neo controls (D1-3 and D1-6) and two SAG-producing lines (D12-1 and D12-8) were chosen to examine their sensitivity to redox compounds by morphological observation. After exposure to 150 μM OP, 200 μM H_2O_2, or 125 μM zinc for 24 hours, the neo-control cells were shrunken and detached, a sign of apoptosis, while SAG-expressing cells appeared morphologically normal. These results indicate that SAG production protects cells from apoptosis induced by redox compounds. Expression of SAG, however, did not offer the protection against copper. No difference in morphological signs of apoptosis was observed with $CuSO_4$ treatment (up to 750 μM) between the vector controls and SAG transfectants. Higher doses induced apoptosis in all lines.

Example 16. SAG expression protects cells from DNA fragmentation

The sensitivity of these SAG-transfected cells to OP-induced apoptosis was examined next by monitoring DNA fragmentation, a hallmark of apoptosis. Subconfluent (80-90%) SAG transfected cells expressing wildtype SAG, SAG mutant-1, SAG mutant-2, or vector control cells, were seeded at 3.5 x 10^6 per 100 mm dish and exposed after 16-24 hours to 150 μM OP, 125 μM zinc sulfate, or 200 μM H_2O_2 for 24 hours. Both detached and attached cells in 2 x 100 mm dishes were harvested and subjected to DNA fragmentation analysis as follows. Cells were collected by centrifugation and lysed with lysis buffer (5 mM Tris-HCL, pH 8; 20 mM EDTA; 0.5% Triton-X100) on ice for 45 minutes. Fragmented DNA in the supernatant of a 14,000 rpm centrifugation (45 minutes at 4°C) was extracted twice with phenol/chloroform and once with chloroform and precipitated by ethanol and salt. The DNA pellet was washed once with 70% ethanol and resuspended in TE buffer with 100 μg/mL RNase at 37°C for 2 hours. The fragmented DNA was separated in 1.8% agarose gel electrophoresis, stained with ethidium bromide, and visualized under ultraviolet light.

OP induced apoptosis in the vector control cells. Less DNA fragmentation was observed in wild type SAG transfected cells compared to control cells. SAG mutant 1, which does not encode the zinc ring-finger motif, did not show any protection against OP-induced DNA fragmentation, whereas SAG mutant 2, which retains the zinc ring finger domain, still showed protection. These results suggest that overexpression of SAG protein protects cells against OP-induced apoptosis, and the zinc ring finger domain is required for this protective activity.

Since SAG protein contains a zinc ring finger motif, the sensitivity of SAG transfectants to zinc treatment was examined next. Zinc induced apoptosis in DLD-1 cells

transfected with the vector only. Induction of apoptosis was limited by SAG overexpression, which showed much less DNA fragmentation than the control lines. This data suggests that the SAG protein binds to and chelates zinc through the zinc ring finger domain and thus provides increased resistance to zinc toxicity compared to non-transfected cells.

Another feature of SAG is the formation of oligomers after exposure to H_2O_2. Cells may be protected from H_2O_2 induced toxicity by SAG oligomerization. SAG-transfected cells were, therefore, treated with H_2O_2 followed by assays for DNA fragmentation. H_2O_2 induced apoptosis in DLD-1 cells. SAG protein overexpression partially protected cells from H_2O_2-induced apoptosis, as evidenced by a reduction in DNA fragmentation. Taken together, these results demonstrate that SAG affords at least some protection against apoptosis induced by redox compounds such as OP and H_2O_2 and also against apoptosis caused by zinc.

Example 17. Antisense SAG expression inhibits tumor cell growth

To test the growth effects induced by SAG expression, DLD-1 cells were transfected with the neo control vector, or vectors expressing SAG, SAG mutants 1 or 2, or antisense SAG, as described above. Neomycin resistant colonies were selected with G418 (600 μg/mL) for 18 days and stained with 50% methanol/10% acetic acid/0.25% Coomassie Blue.

A stable DLD-1 transfectant expressing antisense SAG mRNA (D15-1) was cloned after G418 selection in order to examine potential changes in tumor cell phenotype caused by decreased SAG expression. Subconfluent D15-1 cells, along with the vector control cell (D1-6), and SAG (sense) overexpressing cells (D12-1 and D12-8) were metabolically labeled and subjected to immunoprecipitation using SAG protein antibody as described above. Densitometric quantitation of SAG protein expression using a computing densitometer, (Molecular Dynamics) was performed according to the manufacturer's instructions. The number was calculated by arbitrarily choosing the value from the vector control cell D1-6 as 1. Antisense SAG transfected cells (D15-1) exhibited a 60% reduction in endogenous SAG protein. Monolayer growth of DLD-1 cells was significantly inhibited by antisense SAG transfection. None of the other transfectants were growth-inhibited, as compared to the neo control.

It was next examined whether antisense SAG-transfected cells would exhibit growth inhibition in soft agar. D15-1 cells, along with transfectants expressing wildtype SAG (D12-8), SAG mutant-1 (D3-3), SAG mutant-2 (D4-2), as well as the neo control (D1-3)

were grown in 0.25% agar medium for 14 days. Colonies containing greater than 16 cells were counted. Three independent experiments, each run in duplicate, were performed. Shown is the mean +/- standard error of the mean. As shown in Figure 2, down-regulation of SAG in D15-1 cells did cause significant growth inhibition of DLD-1 cells as reflected by 75% reduction of soft agar colony number when compared to the neo control (D1-3), SAG (sense) expressing line, D12-8, and SAG mutants (D3-3, D4-2).

In a further study, 4 x 10^6 confluent D15-1 cells along with parental DLD-1 cells, the vector control D1-6, and SAG wildtype transfectant D12-1 cells were inoculated subcutaneously into SCID mice (Taconic Farms, Germantown, New York), 10 mice per group. Tumor growth was observed twice a week. The average tumor size/mass for 10 mice was plotted against time post injection up to 24 days. When implanted into SCID mice, antisense expressing line D15-1 failed to form tumors up to 24 days after inoculation, whereas substantial tumor growth was observed in parental DLD-1 cells, the neo control D1-6 cells, and SAG (sense) expressing D12-1 cells (Figure 3). All these experiments demonstrate that downregulation of SAG expression leads to growth inhibition of tumor cells, and further indicates that SAG is a cellular protective molecule.

Example 18. Cancer gene therapy using adenovirus expressing antisense SAG

Since antisense SAG expression has been shown to inhibit tumor growth both *in vitro* and *in vivo* (example 17), SAG can be used as a target for cancer gene therapy. Methods for conducting cancer gene therapy are well known in the art (see Zhang and Fang, Exp. Opin, Invest. Drugs 4: 487-514, 1995 and Zhang et al., Adv. Pharmacol. 32: 289-341, 1995).

Tumor cell lines with endogenous SAG expression, including, but not limited to DLD-1 (colon), Du145 (prostate), G401 (kidney), H2009 (lung) and HONET-1 (nasopharynx), are used to establish the tumor models,. Tumor cells from tissue culture are suspended in PBS at a concentration of 5 x 10^7/mL and stored on ice. 0.2 mL of the cell suspension (containing approximately ten million cells) is subcutaneously injected into the flank of 6- to 8-week-old athymic nude mice and tumors are allowed to grow for 30-40 days or until the average tumor size reaches 5 mm.

Recombinant adenoviral vectors expressing antisense human SAG, driven by the CMV promoter (Ad.CMV-SAG) were produced by co-transfecting a shuttle plasmid (pJM17, circularized Ad5 genome) and a recombinant plasmid (pEC-SAG; a CMV driven plasmid containing left arm of Ad5 genome) into 293 cells.

Tumors are injected with either 0.1 mL of recombinant adenoviral solution (1-5 x 10^{10} pfu/mL) or 0.1 mL of PBS alone as a control. Daily treatment is performed for 2 days and after 1 week without treatment, daily treatment is resumed for 3 days. The tumor size is measured daily for 2 weeks. To test combinatorial therapy with oxygen radical-generating reagents or irradiation, the treated group is subdivided into three sub-groups (10 mice per subgroup): group A receives adenovirus alone (see above); group B receives adenovirus and at the same time receives an intraperitoneal injection of adriamycin (3 mg/kg) an oxygen radical-generating reagent, and group C receives adenovirus plus irradiation at 350cGy of cesium-137. Some tumor-bearing mice will only receive the same dose of adriamycin or irradiation as drug or irradiation controls,.

Expression of antisense SAG blocks endogenous SAG synthesis, which renders tumor cells supersensitive to oxygen radicals. Significant tumor shrinkage in treated tumors with or without drugs or radiation, as compared with the vehicle control, indicates the efficacy of this therapy. The tumors in both control and treated groups can be further examined histologically. Samples can be immediately embedded in optimal cutting temperature compound (Miles, Inc. Elkhart, Indiana) and snap-frozen in liquid nitrogen for frozen section preparation (3-5 μm) for enzymatic staining (e.g., terminal deoxynucleotidyl transferase (Boehringer Manheim, Indianapolis, Indiana) staining for apoptosis) or immunohistochemical staining for expression of the antisense SAG. Alternatively, the samples may be fixed in 10% formalin for histologic sectioning and analyze with hematoxylin-eosin (Sigma, St. Louis, Missouri) staining.

Example 19. SAG functions as a oxygen radical scavenger to prevent oxygen radical induced damages

SAG protein contains 12 cysteine residues and forms disulfide bonds both intermolecularly and intramolecularly after exposure to hydrogen peroxide. SAG protein also binds to heme, which can modulate oxidants by oxidation/reduction of Fe(++). This oxidative buffering activity may qualify SAG as an oxygen radical scavenger.

Yeast cells having deletions in antioxidant enzyme genes [superoxide dismutase (SOD) and catalase (CAT)] are supersensitive to superoxide anion and hydrogen peroxide (Longo et al. (1997), J. Cell Biol. 137:1581-1588). Yeast cells that lack (a) Cu, Zn-SOD, (b) Mn-SOD, (c) both Cu, Zn-SOD and Mn-SOD, and (d) CAT have been transfected with human SAG expression plasmids. Sensitivity of these transfected cells to oxygen radical producing compounds such as paraquat (a superoxide anion generating compound) and

hydrogen peroxide are tested in yeast growth assays and compared to the growth of the same host cells transfected with vector controls. Rescue of these yeast cells from oxygen radical-induced cell killing indicates that SAG is an effective oxygen radical scavenger.

Example 20. Prevention of IL-1β induced brain injury during ischemia by SAG administration

It has been previously shown that middle cerebral artery occlusion in rats causes overexpression of interleukin-1 which induces brain injury by the release of free radicals (Yang et al., Brain Research 751:181-188, (1997)). Two experiments are conducted to test whether SAG, by scavenging free radicals released, will prevent brain damage.

In the first experiment, human SAG is subcloned into an adenovirus vector driven by RSV promoter (AdRSV-SAG). The adenoviral suspension is injected stereotactically into the lateral ventricle to ensure SAG expression in brain. Five days after administration of adenovirus, middle cerebral artery is occluded in animals for 24 hours as described (Yang et al., Brain Research 751:181-188, (1997)). Brain edema (as measured by brain water content) and cerebral infarct size, measured by histological techniques (Yang et al., Stroke 23:1331-1336, (1992)) is determined. As compared to the vector control, any reduction of brain edema and infarction size indicates SAG protection against free radical induced damage.

In the second experiment, middle cerebral artery occlusion is performed with the rat suture model, allowing either permanent (6 hours) or temporary occlusion (3 hours of occlusion and 3 hours of reperfusion) (Yang and Betz, Stroke, 25:1658-1665, (1994)). Rats then receive an injection of purified SAG protein at the size of occlusion. Brain water, ion contents, and infarct volume are measured to determine brain infarction and blood-brain barrier disruption. As compared to injection of the vehicle control, reduction in brain infarction size and blood-brain barrier disruption indicates a SAG protective effect.

Example 21. Human cancer diagnosis using SAG as a marker:

Two SAG deletion mutants in human cancer cell lines originating from colon and testis have been identitifed. Twelve pairs of colon carcinomas and adjacent normal tissues were collected from 12 patients. Genomic DNA and total RNA are isolated from these samples and subjected to PCR amplification. The resulting amplification products are analyzed for detection of SAG deletion mutations by methods well known in the art, including but not limited to RNA protection assays, DNA sequencing, hybridization, and gel

electrophoresis for deletion mutants. Mutations detected in tumor tissues but not in normal adjacent tissues indicate that they are tumor specific mutations and can be used as a diagnostic tool in the clinic for colon as well as testicular carcinomas.

Example 22: The yeast homolog of human SAG gene is essential for yeast growth

To further understand the function of SAG, yeast SAG knock-out mutants were constructed by homologous recombination. The construct used to knockout yeast SAG was made by PCR of a kanamycin cassette from kanMX4 plasmid (Wach et al., Yeast 10:1793-1808, 1994). The primers used for PCR were SAGKanMX4-5: 5′-TTCTCCAGTGGCAGAGAACTTTAAAGAGAAATAGTTCAAC CGTACGCTGCAGGTCGAC-3′ (**SEQ ID 17**), and SAGKanMX4-3: 5′-ACCTCGGTA TGATTTAAATGTTTACGGGCAATTCATTTTT ATCGATGAATTCGAGCTCG-3′ (**SEQ ID 18**). The primer SAGKanMX4-5 consists of yeast SAG DNA sequence (ATCC Accession number Z74876) immediately upstream of the initiation codon ATG (underlined) and the upstream kanamycin cassette sequence at its 3′-end. Primer SAGKanMX4-3 consists of yeast SAG DNA sequence immediately downstream of the stop codon TGA (underlined) and the downstream kanamycin cassette sequence at its 3′-end.

PCR was conducted for 5 cycles at 94°C 1 min, 50°C, 1.5 min, 72°C 2 min, followed by 25 cycles at 94°C, 1 min, 56°C, 1.5 min, 72°C 2 min, followed by a 10 min extension at 72°C. The resulting PCR product (1.5 kb) was gel-purified using Qiaex II gel-purification kit (Qiagen) according to the manufacturer's instruction, and was used to transfect the diploid yeast strain Y21 using the YEASTMAKER yeast Transformation System (ClonTech Laboratory, Inc.) according to the manufacturer's instruction. Following transfection, yeast cells were grown in YPD media (Difco) containing G418 (200 μg/mL, BRL) to select transfectants containing the kanamycin cassette, which have had the yeast SAG deleted by homologous recombination.

Several G418-resistant clones were selected and assayed to determine whether heterozygous or homozygous deletions had been produced. The primers used are SAGPCR-5: 5′-TTCTCCAGTGGCAGAGAAC-3′ (**SEQ ID 19**) and SAGPCR-3: 5′-ATGATTTAAATGTTTACGGGC-3′ (**SEQ ID 20**). These primers constitute fragments of SAGKanMX4-5 and SAGKanMX4-3, respectively, and flank the entire yeast SAG coding region. PCR of wildtype yeast SAG produces a 0.35 kb band, whereas PCR of SAG deletion

mutants give rise to 1.5kb band, consisting of the kanamycin cassette. Both the 0.35 kb and 1.5 kb fragments were generated in all of the clones tested, indicating that heterozygous mutants were produced. Identical knock-out experiments were conducted with haploid yeast cells (InvSC1 from In Vitrogen) and no G418-resistant clone was isolated.

The failure to isolate homozygous yeast SAG deletion mutants suggests that yeast SAG is essential for growth. To confirm this, 12 individual heterozygous yeast strains (y21-ySAG/ySAG::Kan) were sporulated to determine if yeast SAG-kan haploids were viable. The strains were inoculated into minimal potassium acetate sporulation media, supplemented with uracil, lysine, adenine and tryptophan (Kassir, and Simchen, G. Method Enzymol. 194, 94-110, 1991) and grown at 30°C for 7 days. Tetrads was dissected into 4 haploid offspring from each strain. For dissection, a clamp of cells from the sporulation plate was suspended in 100 µL of 1 M glycerol containing 0.5 mg/mL zymolase T20. After 30 min at 37°C, the suspension was diluted with 800 µL sterile water and put on ice. A loop of suspension was struck across a YPD plate and examined under a Zeiss Tetrad microscope for tetrads. The glass microneedle of the scope was used to dissect 4 tetrads from each strain. Two of these four haploid cell should contain wildtype SAG, while the other two should contain a yeast SAG deletion. In all 12 clones, only two out of four dissected cell grew, and none were viable in YPD medium supplemented with G418, indicating that viable cells did not contain the kanamycin cassette or the SAG deletion. The experiment clearly demonstrate that SAG is essential for yeast growth, further demonstrating its evolutionary importance.

To determine if *ySAG* is required for normal growth or simply for germination, *hSAG* was cloned into a yeast expression vector with *URA3* selectable marker. The *hSAG-URA* plasmid was then transformed into heterozygous ySAG knockout cells, and transformants were selected on URA-minus plates. Clones expressing hSAG (measured by Western blot analysis) were sporulated and tetrads were dissected. Viable colonies were then screened on either YPD alone, or YPD+G418, or YPD+5-fluoroorotic acid (5-FOA; used to select against the URA3-containing centromere plasmid (Boeke et al., Mol. Gen. Genet, 1984;197:345). Again the *hSAG-URA3* plasmid complemented the *ySAG::kan* allele, as all four haploids from four individual tetrads grew. When grown on YPD+G418 plates, two haploids from each tetrad die, indicating that they contain the wildtype *ySAG* gene. Other two haploids from each tetrads survived, indicating they contained *ySAG::kan* allele. When these latter colonies were grown on YPD+5-FOA plates, which selects against URA3 plasmid, all failed

to grow, indicating that *ySAG* is essential for normal vegetative growth and not simply for sporulation.

Example 23: Human SAG rescue of yeast SAG knockout phenotype

To examine whether human SAG can rescue death phenotype of yeast SAG knockout, wildtype human SAG, along with the SAG mutants (MM3, sequence ID 25; MM10, sequence ID 39; and MM14, sequence ID 47, Figure 1A) were constructed into a plasmid with Trp selection marker and transfected into heterozygous yeast strain (y21-SAG/ySAG::Kan) as described above. The clones grown in Trp-minus/G418-plus plates were examined by Western blot analysis for SAG expression. The clones expressing human SAG were sporulated and dissected. In 10 wildtype human SAG clones, 3 or 4 haploids are viable. Some of them contain yeast SAG, whereas the others contain ySAG K/O plus human SAG, indicating human wildtype SAG can complement yeast SAG knockout. All three mutant clones (total of 41 tested) gave rise to 1 or 2 haploids and all survival haploids contains yeast SAG, indicating that human SAG mutants cannot complement yeast SAG knockout.

Example 24: SAG binds to metals

Since SAG contains a zinc-ring finger domain, it has the potential to bind with metals. To measure potential metal binding of SAG, electrospray ionization mass spectrometry (ESI-MS) (Fenn et al., 1989) was used to compare the molecular mass of SAG under denaturing and non-denaturing solution conditions (Loo, 1997; Witkowska et al., 1995).

ESI-MS was performed with a double focusing hybrid mass spectrometer (Finnigan MAT 900Q, Bremen, Germany) with a mass-to-charge (m/z) range of 10,000 at 5 kV full acceleration potential. A position-and-time-resolved-ion-counting (PATRIC) scanning array detector was used. An ESI interface based on a heated metal capillary inlet and a low flow micro-EsI source (150 nL/min analyte flowrate) were used (Sannes-Lowery et al., 1997). The metal capillary temperature was maintained around 150-200°C for metal-protein complex studies. Recombinant protein under 7 M urea-denaturing solution was refolded by dialyzing in 50 μM $ZnCl_2$ for 3 days with three changes of buffer. Prior to ESI-MS measurement, the SAG solution was washed with a solution of 10 mM ammonium bicarbonate (pH 7) and 1 mM DTT, and excess zinc was removed by centrifugal ultrafiltration by passing through a 10 kDa molecular weight cut-off centrifugal filtration cartridge (Microcon-10 microconcentrator, Amicon, Beverly, MA). For the ESI-MS

analysis, a small portion of the filtered SAG protein solution was diluted into either a denaturing solvent (80:15:5 acetonitrile:water:acetic acid v/v/v, pH 2.5) or a non-denaturing solution (10 mM ammonium bicarbonate and 1 mM DTT, pH 7).

Zinc binding of SAG was first measured. Under a denaturing acidic solution (pH 2.5 and high organic concentration) where the protein is not expected to retain metal-binding characteristics even in the presence of zinc, the molecular mass of SAG was measured to be 12550, in close agreement with the expected mass for the apo-protein (12552 Da). The ESI-MS analysis of the SAG protein in a non-denaturing aqueous solution (pH 7) resulted in an increase in mass to 12733 and 12800 Da. These masses are consistent for the holo-protein binding 3 and 4 zinc metal ions, respectively.

Copper binding to SAG was also measured. As little as 1 μM $CuSO_4$ in the dialysis solution causes SAG precipitation with a blue (copper) color, suggesting a copper binding. Next, using ESI-MS, the potential copper binding of SAG was measured in a non-denaturing solution described above. Addition of copper acetate to a final concentration of 10 μM resulted in a further inccrease in mass to approximately 12929 Da. However, a precise mass could not be obtained, as a wide distribution of copper adducts appears to bind to SAG protein. Adding copper to higher concentrations resulted in precipitation of the protein.

Example 25: SAG minimizes or prevents LDL oxidation induced by copper ion or a free radical generator

Due to its H_2O_2 buffering and metal binding, it was reasoned that SAG may prevent oxidation of macromolecules induced by metal or free radical generator. An LDL (low density lipoprotein) oxidation induced by copper ion or a free radical generator, AAPH (2,2-azobis-2-amidinopropane hydrochloride), was used as a model to test potential protection activity of SAG against lipid peroxidation.

Lipoproteins (100 μg of protein/mL, Intraocel) were incubated with 10 μM $CuSO_4$ or with 5 mM AAPH for 4 hours at 37°C in the presence of various concentrations of purified SAG protein. AAPH is a water-soluble azo compound that thermally decomposes and generates water soluble peroxyl radicals at a constant rate (Frei et al., 1988). Oxidation was terminated by the addition of 10 μM butylated hydrozytoluence (BHT) and refrigeration at 4°C. The extent of lipoprotein oxidation was measured by the TBARS assay, using malondialdehyde (MDA) for the standard curve, as described (Buege & Aust, 1978).

Copper-induced LDL oxidation, as measured by the formation of thio barbituric acid reactive substances (TBARS), was slightly enhanced by SAG at low concentrations. At higher SAG concentrations, however, a dose-dependent inhibition (up to 90%) of LDL oxidation was observed. Inhibition was heat-resistant since heat-treated (60°C for 15 min) SAG still retains the activity, suggesting that enzymatic activity is not involved. Inhibitory activity was, however, completely or partially abolished by pretreatment of SAG with alkylating reagents NEM and p-hydroxy mercury benzoate (PHMB), respectively. The results indicated that free SH groups in SAG are the major contributors to this activity. Furthermore, metallothionein, a small metal binding protein consisting of 20 cysteine residues out of 61 amino acids (Nordberg & Kojima, 1979) showed a similar inhibitory curve as SAG. Glutathion (GSH), an additional cysteine containing peptide showed a 25% inhibition at a concentration of 100 μM. Inhibition of copper-induced LDL oxidation was, however, not observed in other known antioxidant enzymes such as superoxide dismutase, catalase or other proteins such as BSA, and cytochrome C. These results clearly showed that by binding and chelating copper ion through its free SH groups, SAG prevents copper-initiated free radical reactions leading to LDL oxidation and superoxide or hydrogen peroxide appear not to be involved in the process. To test whether SAG protection against LDL oxidation was solely mediated through copper binding, we initiated LDL oxidation by AAPH, a free radical generator. In this metal-ion free system, SAG also protects LDL oxidation (up to 85%) at a concentration of 59 μM (750 μg/mL). Thus, by metal binding and free radical scavenging, SAG acts as a protector against lipid peroxidation.

Example 26. SAG protects cytochrome C release and caspase activation induced by metal ions

Since cytochrome C release from mitochondria and caspase activation are the key events in apoptosis (Liu et al., 1996; Yang et al., 1997; Li et al., 1997; Hengartner, 1998, for review, see Mignotte & Vayssiere, 1998), the levels of cytochrome C released into cytoplasm and potential activation of caspase upon metal treatments were measured. Treatment of cells with $ZnSO_4$ induces a time-dependent release of cytochrome C in cytoplasm. Compared to the vector control cell (D1-6), the SAG overexpressing cell (D12-1) has much less cytoplasmic release of cytochrome C. Likewise, activation of caspase 7, shown as disappearance of pro-enzyme form, was seen in a time-dependent manner post zinc treatment. More activation was seen in vector control cell (D1-6) than that in the SAG overexpressing

cell (D12-1). A similar result was obtained with CPP32 (caspase 3) activation. A significant difference, however, was not seen in cytochrome C release or caspase activation between D1-6 and D12-1 cells upon copper treatment. This is consistent with the lack of difference in morphological changes between the two lines upon copper treatment, although DNA fragmentation was obvious only in the vector control cells. To further examine potential protection of SAG against metal-induced cytochrome C release and CPP32 activation, cytochrome C release and CPP32 activation was measured in 293 cells transiently transfected with SAG expressing plasmid followed by exposure to copper. A significant amount of cytochrome C started to release 6 hours post $CuSO_4$ (2.0 mM) treatment and lasted up to 12 hours. Expression of SAG delayed cytochrome C release for up to 16 hours. Activation of caspase 7 was seen in the vector control cells 12 hours and 16 hours post copper treatment. No significant activation was seen in SAG transfectants. The similar result was seen with CPP32 antibody. For zinc treatment, no difference was detected in cytochrome C release and caspase activation between control cells and SAG transfectants, consistent with the lack of difference in morphological signs of apoptosis. These results indicate that metal treatment induces cytochrome C release and caspase activation during apoptosis which can be largely prevented or delayed by SAG and there is a good correlation between morphological signs of apoptosis and cytochrome C release/caspase activation.

Example 27: SAG protects against neuronal apoptosis

SAG was transfected into HY5Y human neuroblastoma cells and a few stable lines were selected which expressed exogenous SAG as determined by Western blot. One SAG-transfectant (SYW-20) and a vector control (SYV-3) were used to determine their sensitivity to metal ions, zinc and copper. Treatment with 1.25 mM $CuSO_4$ or 200 μM $ZnSO_4$ for 16 hours induced cell shrinkage and detachment in the neo control cells, but to a less extent in SAG-expressing cells. The morphological difference was more obviously seen with the zinc treatment. To determine the nature of cell death, we performed TUNEL assay, a fluorescein labelling assay of free 3′-OH termini generated from cleavage of genomic DNA during apoptosis.

In Situ cell death assay (TUNEL assay) was performed according to the manufacturer's instructions (Boehringer Mannheim). Briefly, 5 x 10^4 cells were plated into the 8-well glass slides. After treatment with 1.25 mM copper ($CuSO_4$) or 200 μM zinc ($ZnSO_4$) for 16 hours, cells were fixed with 0.5% glutaraldehyde for 10 min, then washed

with PBS twice. The fixed cells were incubated in permeabilization solution (0.1% Triton X-100, 0.1% sodium citrate) for 2 min on ice. The TUNEL reaction mixture (50 µL) was added to samples and incubated for 1 hour at 37°C followed by 3 times wash with PBS. Samples were embedded with antifade prior to analysis under a fluorescence microscope. Substantially more fluorescein staining was seen in the vector control cells after 16 hours treatment with 1.25 mM $CuSO_4$, or 200 µM $ZnSO_4$. The results indicate that expression of SAG protects neuronal cells from apoptosis.

Example 28. SAG stimulates proliferation

To test potential growth stimulation activity, SAG RNA (8 µg/mL or 25 µg/mL), along with the control β-galactosidase (25 µg/mL), was injected into serum-starved NIH 3T3 fibroblast monolayer. Approximately 50 cells attached to the glass coverslip within an etched circle were injected. A 3-hour pulse of [^{3}H]thymidine (5 µCi/mL, Amersham) was performed 10 to 24 hours after injection. Cultures were washed with isotonic phosphate-buffered saline and fixed in 3.7% (vol/vol) formaldehyde. Induction of [^{3}H]thymidine incorporation (an indicator of DNA synthesis) into the nuclei of serum-starved fibroblast cells was obviously observed in SAG-injected cells. In contrast, injection of β-galactosidase does not induce DNA synthesis and no [^{3}H]thymidine incorporation was observed. The results clearly indicate that human SAG has proliferative activity to stimulate cell growth.

Growth promotion activity of SAG was also examined in human neuroblastoma cells (SY5Y), overexpressing hSAG protein by hSAG cDNA transfection. Both the vector-expressing control cells and SAG overexpressing cells were first serum-starved for 48 hours, followed by 3H-thymidine labelling for 16 hours in either serum-starved or 1% serum conditions. Cells were washed, lysed and counted in a liquid scintillation counter for 3H, an assay for the measurement of 3H-thymidine incorporation into DNA (S-phase entry). Compared to the vector control cells, SAG-expressing cells have 10-fold more 3H-thymidine incorporation in both conditions (serum-free or 1% serum), indicating that SAG stimulates cell proliferation/growth.

Growth promotion activity of SAG was also examined in yeast. As described in Example 22, the yeast homolog of human SAG gene is essential for yeast growth. To correlate yeast growth rate with SAG expression, hSAG expressing plasmid was constructed under control of Gal promoter. The plasmid was transformed into heterozygous ySAG knockout and transformants were sporulated and dissected. Haploid ySAG knockout clone

that contained hSAG plasmid was identified and analyzed. In the uninduced condition, little SAG expression due to the leakness of the promoter led to formation a tiny clone compared to the full size wildtype clone. Under induced condition, SAG expression level increased and clone size also increased. This experiment clearly demonstrated that SAG promotes cell growth in a dose-dependent manner.

It is to be understood that the invention is not to be limited to the exact details of operation, or to the exact compounds, compositions, methods, procedures or embodiments shown and described, as obvious modifications and equivalents will be apparent to one skilled in the art, and the invention is therefore to be limited only by the full scope of the appended claims.

I claim

1. An isolated and purified DNA sequence substantially similar to the DNA sequence shown in SEQ ID 1.

2. An isolated and purified DNA sequence that hybridizes to the DNA sequence shown in SEQ ID 1 under high stringency hybridization conditions.

3. An isolated and purified DNA sequence that consists essentially of the DNA sequence shown in SEQ ID 1.

4. A recombinant DNA molecule comprising the isolated and purified DNA sequence of Claim 1, 2, or 3 subcloned into an extra-chromosomal vector.

5. A recombinant host cell comprising a host cell transfected with the recombinant DNA molecule of Claim 4.

6. A recombinant host cell deposited with the ATCC under accession number 98402.

7. An isolated and purified DNA sequence substantially similar to the DNA sequence shown in SEQ ID 3.

8. An isolated and purified DNA sequence that hybridizes to the DNA sequence shown in SEQ ID 3 under high stringency hybridization conditions.

9. An isolated and purified DNA sequence that consists essentially of the DNA sequence shown in SEQ ID 3.

10. A recombinant DNA molecule comprising the isolated and purified DNA sequence of Claim 7, 8, or 9 subcloned into an extra-chromosomal vector.

11. A recombinant host cell comprising a host cell transfected with the recombinant DNA molecule of Claim 10.

12. A recombinant host cell deposited with the ATCC under accession number 98403.

13. A recombinant host cell deposited with the ATCC under accession number 98404.

14. A recombinant host cell deposited with the ATCC under accession number 98405.

15. An isolated and purified DNA sequence selected from the group consisting of SEQ ID 11, SEQ ID 13, SEQ ID 21, SEQ ID 23, SEQ ID 25, SEQ ID 27, SEQ ID 29, SEQ ID 31, SEQ ID 33, SEQ ID 35, SEQ ID 37, SEQ ID 39, SEQ ID 41, SEQ ID 43, SEQ ID 45, SEQ ID 47, and SEQ ID 49.

16. A recombinant DNA molecule comprising an isolated and purified DNA sequence of Claim 15, subcloned into an extra-chromosomal vector.

17. A recombinant host cell comprising a host cell transfected with a recombinant DNA molecule of Claim 16.

18. A substantially purified recombinant polypeptide, wherein the amino acid sequence of

the substantially purified recombinant polypeptide is substantially similar to the amino acid sequence shown in SEQ ID 2.

19. A substantially purified recombinant polypeptide, wherein the amino acid sequence of the substantially purified recombinant polypeptide consists essentially of the amino acid sequence shown in SEQ ID 2.

20. A substantially purified recombinant polypeptide, wherein the amino acid sequence of the substantially purified recombinant polypeptide is substantially similar to the amino acid sequence shown in SEQ ID 4.

21. A substantially purified recombinant polypeptide, wherein the amino acid sequence of the substantially purified recombinant polypeptide consists essentially of the amino acid sequence shown in SEQ ID 4.

22. A substantially purified recombinant polypeptide, wherein the amino acid sequence of the polypeptide is selected from the group consisting of SEQ ID 12, SEQ ID 14, SEQ ID 22, SEQ ID 24, SEQ ID 26, SEQ ID 28, SEQ ID 30, SEQ ID 32, SEQ ID 34, SEQ ID 36, SEQ ID 38, SEQ ID 40, SEQ ID 42, SEQ ID 44, SEQ ID 46, SEQ ID 48, and SEQ ID 50.

23. An antibody that selectively binds polypeptides with an amino acid sequence substantially similar to the amino acid sequence of Claim 18, 19, 20, 21 or 22.

24. A method of detecting SAG protein in cells, comprising contacting cells with the antibody of Claim 23 and incubating the cells in a manner that allows for detection of the SAG protein-antibody complex.

25. A diagnostic assay for detecting cells containing SAG mutations, comprising isolating total genomic DNA from the cell and subjecting the genomic DNA to PCR amplification using primers derived from the isolated and purified DNA sequence of Claim 1, 2, 3, 7, 8, 9, or 15, and determining whether the resulting PCR product contains a mutation.

26. A diagnostic assay for detecting cells containing SAG mutations, comprising isolating total cell RNA, subjecting the RNA to reverse transcription-PCR amplification using primers derived from the isolated and purified DNA sequence of Claim 1, 2, 3, 7, 8, 9, or 15 and determining whether the resulting PCR product contains a mutation.

27. A method of isolating RNA containing stretches of polyA or polyC residues, comprising

(a) contacting an RNA sample with SAG protein in RNA binding buffer in the presence of a reducing agent;

(b) incubating the RNA-SAG protein mixture with the antibody of Claim 23;

(c) isolating the antibody-SAG protein-RNA complexes; and

(d) purifying the RNA away from the antibody-SAG protein complex.

28. A method of isolating RNA containing stretches of polyU residues, comprising

(a) contacting an RNA sample with SAG protein in RNA binding buffer in the absence of reducing agents;

(b) incubating the RNA-SAG protein mixture with the antibody of Claim 23;

(c) isolating the antibody-SAG protein-RNA complexes; and

(d) purifying the RNA away from the antibody-SAG protein complex.

29. A method for isolating genes induced during cell apoptosis, comprising:

(a) treating one set of cells with OP and not treating a control set of cells;

(b) isolating RNA from each set of cells;

(c) subjecting the RNA from each set of cells to the differential display procedure, wherein the RNA is reverse transcribed into cDNA and the cDNA is subjected to the polymerase chain reaction;

(d) identifying cDNAs that are expressed in the OP-treated set of cells and not in the control set of cells; and

(e) cloning the OP-induced cDNAs.

30. A method for protecting cells from apoptosis induced by redox reagents, comprising introducing into the cells an expression vector comprising the isolated and purified DNA sequence of Claim 1, 2, 3, 7, 8, 9, or 15, which is operatively linked to a DNA sequence that promotes the high level expression of the isolated and purified DNA sequence in the cells.

31. A method for inhibiting the growth of tumor cells, comprising introducing into the tumor cells an expression vector comprising the isolated and purified DNA sequence of Claim 1, 2, 3, 7, 8, 9, or 15, which is operatively linked to a DNA sequence that promotes the high level expression of the antisense strand of the isolated and purified DNA sequence in the cells.

32. A method for purifying SAG protein from bacterial cells comprising:

a) transfecting a bacterial host cell with a vector comprising the isolated and purified DNA sequence of Claim 1, 2, 3, 7, 8, 9, or 15 operatively linked to a promoter capable of directing gene expression in a bacterial host cell;

b) inducing expression of the isolated and purified DNA sequence in the bacterial cells;

c) lysing the bacterial cells;

d) isolating bacterial inclusion bodies;

e) purifying SAG protein from the isolated inclusion bodies.

33. A pharmaceutical composition comprising the substantially purified recombinant polypeptide of Claim 18, 19, 20, 21, or 22 and a pharmaceutically acceptable carrier.

34. The pharmaceutical composition of Claim 33 wherein the substantially purified recombinant polypeptide comprises an oligomer.

35. A method of oxygen radical scavenging in an organism comprising administering an oxygen radical -reducing amount of the pharmaceutical composition of Claim 33 or 34 to the organism.

36. A method of promoting the healing of a wound comprising administering the DNA sequence of Claim 1 to cells associated with the wound.

37. A method of promoting or inhibiting the growth of plant cells comprising administering the DNA sequence of Claim 1 or a DNA sequence which is complementary to the DNA sequence of Claim 1 to plant cells.

Docket No.
5650-01-MJA

Declaration and Power of Attorney For Patent Application

English Language Declaration

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name,

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled
SAG: SENSITIVE TO APOPTOSIS GENE

the specification of which

(check one)

☒ is attached hereto.

☐ was filed on _____ as United States Application No. or PCT International Application Number _____

and was amended on _____
(if applicable)

I hereby state that I have reviewed and understand the contents of the above identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose to the United States Patent and Trademark Office all information known to me to be material to patentability as defined in Title 37, Code of Federal Regulations, Section 1.56.

I hereby claim foreign priority benefits under Title 35, United States Code, Section 119(a)-(d) or Section 365(b) of any foreign application(s) for patent or inventor's certificate, or Section 365(a) of any PCT International application which designated at least one country other than the United States, listed below and have also identified below, by checking the box, any foreign application for patent or inventor's certificate or PCT International application having a filing date before that of the application on which priority is claimed.

Prior Foreign Application(s)			Priority Not Claimed
_____ (Number)	_____ (Country)	_____ (Day/Month/Year Filed)	☐
_____ (Number)	_____ (Country)	_____ (Day/Month/Year Filed)	☐
_____ (Number)	_____ (Country)	_____ (Day/Month/Year Filed)	☐

I hereby claim the benefit under 35 U.S.C. Section 119(e) of any United States provisional

60/068,179	**December 19, 1997**
(Application Serial No.)	(Filing Date)
60/099,840	**September 11, 1998**
(Application Serial No.)	(Filing Date)
(Application Serial No.)	(Filing Date)

I hereby claim the benefit under 35 U. S. C. Section 120 of any United States application(s), or Section 365(c) of any PCT International application designating the United States, listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States or PCT International application in the manner provided by the first paragraph of 35 U.S.C. Section 112, I acknowledge the duty to disclose to the United States Patent and Trademark Office all information known to me to be material to patentability as defined in Title 37, C. F. R., Section 1.56 which became available between the filing date of the prior application and the national or PCT International filing date of this application:

PCT/US98/26705	**December 15, 1998**	**Pending**
(Application Serial No.)	(Filing Date)	(Status) (patented, pending, abandoned)
(Application Serial No.)	(Filing Date)	(Status) (patented, pending, abandoned)
(Application Serial No.)	(Filing Date)	(Status) (patented, pending, abandoned)

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

POWER OF ATTORNEY: As a named inventor, I hereby appoint the following attorney(s) and/or agent(s) to prosecute this application and transact all business in the Patent and Trademark Office connected therewith. *(list name and registration number)*

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Second inventor's signature Date
Residence
Citizenship
Post Office Address

SEQUENCE LISTING

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(ii) TITLE OF INVENTION: Sensitive to Apoptosis Gene (SAG)

(iii) NUMBER OF SEQUENCES: 50

(iv) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1140 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:17..355

(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION:17..355

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION:1..1140
(D) OTHER INFORMATION:/note= "Mouse SAG"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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GTTCTGCGCC GCCGCC ATG GCC GAC GTG GAG GAC GGC GAG GAA CCC TGC          49
                  Met Ala Asp Val Glu Asp Gly Glu Glu Pro Cys
                    1               5                  10

GTC CTT TCT TCG CAC TCC GGG AGC GCA GGC TCC AAG TCG GGA GGC GAC        97
Val Leu Ser Ser His Ser Gly Ser Ala Gly Ser Lys Ser Gly Gly Asp
            15                  20                  25
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AAG ATG TTC TCT CTC AAG AAG TGG AAC GCG GTA GCC ATG TGG AGC TGG        145
Lys Met Phe Ser Leu Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp
          30                  35                  40
GAC GTT GAG TGC GAT ACC TGT GCC ATC TGC AGG GTC CAG GTG ATG GAT        193
Asp Val Glu Cys Asp Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp
     45                  50                  55

GCC TGC CTT CGA TGT CAA GCT GAA AAC AAG CAA GAG GAC TGT GTT GTG        241
Ala Cys Leu Arg Cys Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val
 60                  65                  70                  75

GTC TGG GGA GAG TGT AAC CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG        289
Val Trp Gly Glu Cys Asn His Ser Phe His Asn Cys Cys Met Ser Leu
                 80                  85                  90

TGG GTG AAA CAG AAC AAT CGC TGC CCT CTG TGC CAG CAG GAC TGG GTA        337
Trp Val Lys Gln Asn Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val
            95                  100                 105

GTC CAA AGA ATC GGC AAA TGAGAGGTGG CCCAGGCGCT CCTGGTGTGG               385
Val Gln Arg Ile Gly Lys
        110

TTGCTGACCC TGGACAAAGA CTAAACACTG CAGGGGATTC ATCCTTGAGA GAGAGAGGAT      445

GCTGTGCGCC TTTGAGACTC ACCAAAGGCT TGCTTTATTA ATTTGTCTGT TTAGTTTTGG      505

GAAATTCTCT ACAATTAAGA TAATTTGTTA AAAATGGCCT TTCCTACCTC TGGTGTGTGT      565

GTGTGATACG AATGCATAGA AGAGCGAGAA CACCAGAAAA TGATCTTTGT TTATCTGTAC      625

CCACGACTGG AACATTGTGT TCACAGAAGA ACATTGTTTG TGTTTATGCT TGAGGGTTAA      685

AAAATAGATA AACGAATGTT ACAGTAACAA ATAAAATGCA TTGAAAAGCC GACTCCTCCT      745

AATCCTTTTT GTGTTGGGAG AGAGGCAAGC GAGGCCACCC TGCTGTCTTC ATTTGCTGTG      805

AATGAGGATT TTAACCTGCA CTCAGTGAAG AGGCGTAACT GTCGGGTAAA CTGTAATATG      865

GCGTAACTGT CGGGTAAACG GCTTTGTCTC CTGACTTCTC CATCTTTGAC TTGGCCAGGA      925

AGCCTGGATT GTTCAACCAC TTAGTTCTAA AGAACTGTTT TCTGTTTTTG CCGAAGGTTG      985

TATTGTATGT TTTAGTCAAA AATATTAGTA GGAAAATGGC TTACTAGTAT AACACTGAAG     1045

TTCATTATGC AATGTTTTAA TAAAATATTG TGCTTTGAGT TATTAAAGTT TGATATATAC     1105

TCTTAAAATC ATTAAACTAA TTCATCAATT AAATG                                1140
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(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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Met Ala Asp Val Glu Asp Gly Glu Glu Pro Cys Val Leu Ser Ser His
 1               5                  10                  15

Ser Gly Ser Ala Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
            20                  25                  30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
        35                  40                  45

Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
    50                  55                  60

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
65                  70                  75                  80

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
                85                  90                  95

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
            100                 105                 110

Lys
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(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 754 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:1..339

(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION:1..339

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION:1..754
(D) OTHER INFORMATION:/note= "Human SAG"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

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ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC        48
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
 1               5                  10                  15

TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC        96
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
            20                  25                  30

AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT       144
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Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
        35                  40                  45

ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT      192
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
     50                  55                  60

CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT      240
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
 65                  70                  75                  80

AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC      288
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
                85                  90                  95

AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC      336
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
            100                 105                 110

AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTCAGAG CCCTGGTGGA           389
Lys

TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG    449

GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTTT    509

ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC    569

TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT    629

GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT    689

TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT    749

TTAAA                                                                754
```

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

```
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
  1               5                  10                  15

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
            20                  25                  30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
        35                  40                  45

Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
     50                  55                  60
```

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
65 70 75 80

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
85 90 95

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
100 105 110

Lys

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide P1 downstream primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

AAGCTTTTTT TTTTTTTR 18

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligonucleotide: P2 upstream primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

AAGCTTNNNN NNN 13

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligonucleotide SAG TA.01"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CGGGATCCCC ATGGCCGACG TGAGG 25

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide SAG T.02"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

CGGGATCCTC ATTTGCCGAT TCTTTG 26

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide P.01"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

TATGGCTAGC ATGGCCGACG TGGAGG 26

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Gln Asn Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 747 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:1..270

(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION:1..270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

```
ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC        48
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
 1               5                  10                  15

TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC        96
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
            20                  25                  30

AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT       144
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
        35                  40                  45

ACG TGC GCC ATC TGC AGG GTC CAG ATG CCT GTC TTA GAT GTC AAG CTG       192
Thr Cys Ala Ile Cys Arg Val Gln Met Pro Val Leu Asp Val Lys Leu
    50                  55                  60

AAA ACA AAC AAG AGG ACT GTG TTG TGG TCT GGG GAG AAT GTA ATC ATT       240
Lys Thr Asn Lys Arg Thr Val Leu Trp Ser Gly Glu Asn Val Ile Ile
65                  70                  75                  80

CCT TCC ACA ACT GCT GCA TGT CCC TGT GGG TGAAACAGAA CAATCGCTGC        290
Pro Ser Thr Thr Ala Ala Cys Pro Cys Gly
                85                  90

CCTCTCTGCC AGCAGGACTG GGTGGTCCAA AGAATCGGCA AATGAGAGTG GTTAGAAGGC    350

TTCTTAGCGC AGTTGTTCAG AGCCCTGGTG GATCTTGTAA TCCAGTGCCC TACAAAGGCT    410

AGAACACTAC AGGGGATGAA TTCTTCAAAT AGGAGCCGAT GGATCTGTGG TCTTTGGACT    470

CATCAAAGCC TTGGTTAGCA TTTGTCAGTT TTATCTTCAG AAATTCTCTG TGATTAAGAA    530

GATAATTTAT TAAAGGTGGT CCTTCCTACC TCTGTGGTGT GTGTCGCGCA CACAGCTTAG    590

AAGTGCTATA AAAAAGGAAA GAGCTCCAAA TTGAATCACC TTATAATTTA CCCATTTCTA    650

TACAACAGGC AGTGGAAGCA GTTTCGAGAC TTTTTCGATG CTTATGGTTG ATCAGTTAAA    710
```

AAAGAATGTT ACAGTAACAA ATAAAGTGCA GTTTAAA 747

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 90 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

```
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
 1               5                  10                  15

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
            20                  25                  30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
        35                  40                  45

Thr Cys Ala Ile Cys Arg Val Gln Met Pro Val Leu Asp Val Lys Leu
    50                  55                  60

Lys Thr Asn Lys Arg Thr Val Leu Trp Ser Gly Glu Asn Val Ile Ile
65                  70                  75                  80

Pro Ser Thr Thr Ala Ala Cys Pro Cys Gly
                85                  90
```

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 706 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:1..291

(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION:1..291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

```
ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC      48
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
 1               5                  10                  15

TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC      96
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
            20                  25                  30
```

```
AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT        144
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
         35                  40                  45

ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GTG GTC TGG GGA GAA TGT        192
Thr Cys Ala Ile Cys Arg Val Gln Val Met Val Val Trp Gly Glu Cys
     50                  55                  60

AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC        240
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
 65                  70                  75                  80

AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC        288
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
                 85                  90                  95

AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTCAGAG CCCTGGTGGA             341
Lys

TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG      401

GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTTT      461

ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC      521

TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT      581

GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT      641

TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT      701

TTAAA                                                                  706
```

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 97 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

```
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
 1               5                  10                  15

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
            20                  25                  30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
        35                  40                  45

Thr Cys Ala Ile Cys Arg Val Gln Val Met Val Val Trp Gly Glu Cys
    50                  55                  60

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
65                  70                  75                  80
```

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
85 90 95

Lys

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide hSAG. M1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

GCCATCTGCA GGGTCCAG 18

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide SAG T.02L"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

GGATCCTCAT TTGCCGATTC TTTGGAC 27

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide SAGKanMX4-5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

TTCTCCAGTG GCAGAGAACT TTAAAGAGAA ATAGTTCAAC CGTACGCTGC AGGTCGAC 58

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide SAGKan MX 4-3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

ACCTCGGTAT GATTTAAATG TTTACGGGCA ATTCATTTTT ATCGATGAAT TCGAGCTCG 59

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide SAG pcr 5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

TTCTCCAGTG GCAGAGAAC 19

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide SAG pcr 3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

ATGATTTAAA TGTTTACGGG C 21

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 754 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:1..339

(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

```
ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC        48
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
  1               5                  10                  15

TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC        96
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
             20                  25                  30

AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT       144
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
         35                  40                  45

ACG AGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT       192
Thr Ser Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
     50                  55                  60

CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT       240
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
 65                  70                  75                  80

AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC       288
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
                 85                  90                  95

AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC       336
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
            100                 105                 110

AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTCAGAG CCCTGGTGGA            389
Lys

TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG     449

GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTTT     509

ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC     569

TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT     629

GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT     689

TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT     749

TTAAA                                                                 754
```

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

```
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
 1               5                  10                  15

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
            20                  25                  30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
        35                  40                  45

Thr Ser Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
    50                  55                  60

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
65                  70                  75                  80

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
                85                  90                  95

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
            100                 105                 110

Lys
```

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 754 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:1..339

(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

```
ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC      48
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
 1               5                  10                  15
```

```
TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC          96
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
             20                  25                  30

AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT         144
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
         35                  40                  45

ACG TGC GCC ATC AGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT         192
Thr Cys Ala Ile Ser Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
     50                  55                  60

CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT         240
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
 65                  70                  75                  80

AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC         288
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
                 85                  90                  95

AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC         336
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
            100                 105                 110

AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTCAGAG CCCTGGTGGA              389
Lys

TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG       449

GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTTT       509

ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC       569

TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT       629

GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT       689

TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT       749

TTAAA                                                                  754
```

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

```
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
 1               5                  10                  15

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
             20                  25                  30
```

```
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
         35                  40                  45

Thr Cys Ala Ile Ser Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
     50                  55                  60

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
 65                  70                  75                  80

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
                 85                  90                  95

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
            100                 105                 110

Lys
```

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 754 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:1..339

(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

```
ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC        48
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
  1               5                  10                  15

TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC        96
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
             20                  25                  30

AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT       144
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
         35                  40                  45

ACG AGC GCC ATC AGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT       192
Thr Ser Ala Ile Ser Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
     50                  55                  60

CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT       240
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
 65                  70                  75                  80

AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC       288
```

```
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
                 85                  90                  95

AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC      336
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
            100                 105                 110

AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTCAGAG CCCTGGTGGA          389
Lys

TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG   449

GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTTT   509

ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC   569

TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT   629

GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT   689

TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT   749

TTAAA                                                               754
```

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

```
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
  1               5                  10                  15

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
             20                  25                  30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
         35                  40                  45

Thr Ser Ala Ile Ser Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
     50                  55                  60

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
 65                  70                  75                  80

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
                 85                  90                  95

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
            100                 105                 110

Lys
```

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 754 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:1..339

(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

```
ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC        48
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
  1               5                  10                  15

TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC        96
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
             20                  25                  30

AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT       144
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
         35                  40                  45

ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC AGT CTT AGA TGT       192
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Ser Leu Arg Cys
     50                  55                  60

CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT       240
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
 65                  70                  75                  80

AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC       288
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
                 85                  90                  95

AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC       336
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
            100                 105                 110

AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTCAGAG CCCTGGTGGA            389
Lys

TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG     449

GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTTT     509

ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC     569

TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT     629
```

GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT 689

TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT 749

TTAAA 754

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
1 5 10 15

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
20 25 30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
35 40 45

Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Ser Leu Arg Cys
50 55 60

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
65 70 75 80

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
85 90 95

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
100 105 110

Lys

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 754 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:1..339

(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

```
ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC        48
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
  1               5                  10                  15

TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC        96
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
             20                  25                  30

AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT       144
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
         35                  40                  45

ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT       192
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
     50                  55                  60

CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA AGT       240
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Ser
 65                  70                  75                  80

AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC       288
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
                 85                  90                  95

AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC       336
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
            100                 105                 110

AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTCAGAG CCCTGGTGGA            389
Lys

TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG     449

GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTTT     509

ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC     569

TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT     629

GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT     689

TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT     749

TTAAA                                                                 754
```

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

```
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
  1               5                  10                  15
```

```
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
            20                  25                  30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
        35                  40                  45

Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
    50                  55                  60

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Ser
65                  70                  75                  80

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
                85                  90                  95

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
            100                 105                 110

Lys
```

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 754 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:1..339

(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

```
ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC      48
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
  1               5                  10                  15

TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC      96
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
            20                  25                  30

AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT     144
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
        35                  40                  45

ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT     192
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
    50                  55                  60

CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT     240
```

```
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
 65                  70                  75                  80

AAT AAA TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC      288
Asn Lys Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
                 85                  90                  95

AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC      336
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
            100                 105                 110

AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTCAGAG CCCTGGTGGA           389
Lys

TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG    449

GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTTT    509

ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC    569

TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT    629

GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT    689

TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT    749

TTAAA                                                                754
```

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

```
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
  1               5                  10                  15

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
             20                  25                  30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
         35                  40                  45

Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
     50                  55                  60

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
 65                  70                  75                  80

Asn Lys Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
                 85                  90                  95

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
            100                 105                 110
```

Lys

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 754 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:1..339

(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

```
ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC        48
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
  1               5                  10                  15

TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC        96
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
             20                  25                  30

AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT       144
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
         35                  40                  45

ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT       192
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
     50                  55                  60

CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT       240
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
 65                  70                  75                  80

AAT CAT TCC TTC AAG AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC       288
Asn His Ser Phe Lys Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
                 85                  90                  95

AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC       336
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
            100                 105                 110

AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTCAGAG CCCTGGTGGA            389
Lys

TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG     449

GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTTT     509
```

ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC 569

TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT 629

GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT 689

TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT 749

TTAAA 754

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
1 5 10 15

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
20 25 30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
35 40 45

Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
50 55 60

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
65 70 75 80

Asn His Ser Phe Lys Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
85 90 95

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
100 105 110

Lys

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 754 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:1..339

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

```
ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC        48
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
  1               5                  10                  15

TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC        96
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
             20                  25                  30

AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT       144
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
         35                  40                  45

ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT       192
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
     50                  55                  60

CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT       240
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
 65                  70                  75                  80

AAT CAT TCC TTC CAC AAC TGC AGC ATG TCC CTG TGG GTG AAA CAG AAC       288
Asn His Ser Phe His Asn Cys Ser Met Ser Leu Trp Val Lys Gln Asn
                 85                  90                  95

AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC       336
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
            100                 105                 110

AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTCAGAG CCCTGGTGGA            389
Lys

TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG     449

GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTTT     509

ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC     569

TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT     629

GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT     689

TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT     749

TTAAA                                                                 754
```

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

```
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
 1               5                  10                  15

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
            20                  25                  30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
        35                  40                  45

Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
    50                  55                  60

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
65                  70                  75                  80

Asn His Ser Phe His Asn Cys Ser Met Ser Leu Trp Val Lys Gln Asn
                85                  90                  95

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
            100                 105                 110

Lys
```

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 754 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:1..339

(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

```
ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC      48
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
 1               5                  10                  15

TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC      96
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
            20                  25                  30

AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT     144
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
        35                  40                  45

ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT     192
```

```
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
     50                  55                  60

CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT      240
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
 65                  70                  75                  80

AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC      288
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
                 85                  90                  95

AAT CGC AGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC      336
Asn Arg Ser Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
            100                 105                 110

AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTCAGAG CCCTGGTGGA           389
Lys

TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG    449

GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTTT    509

ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC    569

TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT    629

GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT    689

TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT    749

TTAAA                                                                754
```

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

```
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
  1               5                  10                  15

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
             20                  25                  30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
         35                  40                  45

Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
     50                  55                  60

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
 65                  70                  75                  80

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
                 85                  90                  95
```

```
Asn Arg Ser Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
            100                 105                 110

Lys
```

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 754 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:1..339

(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

```
ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC        48
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
  1               5                  10                  15

TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC        96
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
             20                  25                  30

AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT       144
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
         35                  40                  45

ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT       192
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
     50                  55                  60

CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT       240
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
 65                  70                  75                  80

AAT AAA TCC TTC AAG AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC       288
Asn Lys Ser Phe Lys Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
                 85                  90                  95

AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC       336
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
            100                 105                 110

AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTCAGAG CCCTGGTGGA            389
Lys
```

TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG 449

GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTTT 509

ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC 569

TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT 629

GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT 689

TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT 749

TTAAA 754

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
1 5 10 15

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
20 25 30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
35 40 45

Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
50 55 60

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
65 70 75 80

Asn Lys Ser Phe Lys Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
85 90 95

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
100 105 110

Lys

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 754 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION:1..339

(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

```
ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC        48
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
  1               5                  10                  15

TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC        96
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
             20                  25                  30

AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT       144
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
         35                  40                  45

ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA AGT       192
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Ser
     50                  55                  60

CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT       240
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
 65                  70                  75                  80

AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC       288
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
                 85                  90                  95

AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC       336
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
            100                 105                 110

AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTCAGAG CCCTGGTGGA            389
Lys

TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG     449

GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTTT     509

ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC     569

TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT     629

GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT     689

TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT     749

TTAAA                                                                 754
```

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

```
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
 1               5                  10                  15

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
            20                  25                  30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
        35                  40                  45

Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Ser
    50                  55                  60

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
65                  70                  75                  80

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
                85                  90                  95

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
            100                 105                 110

Lys
```

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 754 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:1..339

(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

```
ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC      48
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
 1               5                  10                  15

TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC      96
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
            20                  25                  30

AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT     144
```

```
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
        35                  40                  45

ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT      192
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
     50                  55                  60

CAA GCT GAA AAC AAA CAA GAG GAC AGT GTT GTG GTC TGG GGA GAA TGT      240
Gln Ala Glu Asn Lys Gln Glu Asp Ser Val Val Val Trp Gly Glu Cys
 65                  70                  75                  80

AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC      288
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
                 85                  90                  95

AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC      336
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
            100                 105                 110

AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTCAGAG CCCTGGTGGA           389
Lys

TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG    449

GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTTT    509

ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC    569

TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT    629

GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT    689

TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT    749

TTAAA                                                                754
```

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

```
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
  1               5                  10                  15

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
            20                  25                  30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
        35                  40                  45

Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
     50                  55                  60
```

```
Gln Ala Glu Asn Lys Gln Glu Asp Ser Val Val Val Trp Gly Glu Cys
 65                  70                  75                  80

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
                 85                  90                  95

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
            100                 105                 110

Lys
```

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 754 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:1..339

(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

```
ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC      48
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
  1               5                  10                  15

TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC      96
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
            20                  25                  30

AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT     144
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
        35                  40                  45

ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC AGT CTT AGA AGT     192
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Ser Leu Arg Ser
    50                  55                  60

CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT     240
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
 65                  70                  75                  80

AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC     288
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
                85                  90                  95

AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC     336
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
            100                 105                 110
```

AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTCAGAG CCCTGGTGGA 389
Lys

TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG 449

GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTTT 509

ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC 569

TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT 629

GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT 689

TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT 749

TTAAA 754

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
1 5 10 15

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
20 25 30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
35 40 45

Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Ser Leu Arg Ser
50 55 60

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
65 70 75 80

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
85 90 95

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
100 105 110

Lys

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 754 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:1..339

(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

```
ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC        48
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
  1               5                  10                  15

TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC        96
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
             20                  25                  30

AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT       144
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
         35                  40                  45

ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT       192
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
     50                  55                  60

CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT       240
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
 65                  70                  75                  80

AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC       288
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
                 85                  90                  95

AAT CGC AGC CCT CTC AGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC       336
Asn Arg Ser Pro Leu Ser Gln Gln Asp Trp Val Val Gln Arg Ile Gly
            100                 105                 110

AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTCAGAG CCCTGGTGGA            389
Lys

TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG     449

GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTTT     509

ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC     569

TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT     629

GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT     689

TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT     749

TTAAA                                                                 754
```

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

```
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
 1               5                  10                  15

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
            20                  25                  30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
        35                  40                  45

Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
    50                  55                  60

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
65                  70                  75                  80

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
                85                  90                  95

Asn Arg Ser Pro Leu Ser Gln Gln Asp Trp Val Val Gln Arg Ile Gly
            100                 105                 110

Lys
```

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 754 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:1..339

(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

```
ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC      48
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
 1               5                  10                  15
```

```
TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC          96
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
             20                  25                  30

AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG AGC GAT         144
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Ser Asp
         35                  40                  45

ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT         192
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
     50                  55                  60

CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT         240
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
 65                  70                  75                  80

AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC         288
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
                 85                  90                  95

AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC         336
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
            100                 105                 110

AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTCAGAG CCCTGGTGGA              389
Lys

TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG       449

GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTTT       509

ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC       569

TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT       629

GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT       689

TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT       749

TTAAA                                                                  754
```

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

```
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
 1               5                  10                  15

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
            20                  25                  30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Ser Asp
        35                  40                  45
```

```
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
     50                  55                  60

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
 65                  70                  75                  80

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
                 85                  90                  95

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
            100                 105                 110

Lys
```